

WO 00/15838

PCT/EP99/07376

1183

SEQUENCE LISTING

<110> Hoechst Marion Roussel

<120> ESSENTIAL GENES FROM C. ALBICANS AND A METHOD FOR
SCREENING ANTIMYCOTIC SUBSTANCES USING SAID GENES

<130> SEQID01

<140>

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<160> 1

<170> PatentIn Ver. 2.1

<210> 1

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:probe

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atgggtatat tgaatatgac tcttgattca tttagtgatg gtgggaaaca ttttggaaaa 240
gaactagata atattgtgaa gcaggcagag aaattagtca gtgagggtgc tacgattatt 300
gacattggag gagtttccac acgaccagga agtggtgaac ccactgagga agaagaattg 360
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SEQUENCE LISTING

<110> Hoechst Marion Roussel

<120> ESSENTIAL GENES FROM C. ALBICANS AND A METHOD FOR
SCREENING ANTIMYCOTIC SUBSTANCES USING SAID GENES

<130> SEQID02

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<170> PatentIn Ver. 2.1

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Ile	Thr	Gly	Lys	Asp	Ala	Trp	Asn	Arg	Pro	Thr	Pro	Gln	Pro	Ile	Thr	
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ata	tca	tta	tct	ttc	aat	act	gat	ttc	cat	aag	gca	tcg	gaa	ttg	gat	144
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5183

Ser Arg Leu Pro Val Lys Asp Asn Ile Leu Lys Phe Asp Gln Ile Asn	
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645 650 655

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660 665 670

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<213> Candida albicans

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Gly Ser Ile Val Asp Val Thr Ile Lys Ser Leu Lys Ser Glu Ile Arg
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Val Glu Ala Leu Val Ser Lys Ile Gly Gln Leu Thr Phe Gln Lys Tyr
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Asp Gly Val Ala Glu Val Val Ala Thr Val Thr Lys Pro Asn Ala Phe
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Ser His Val Glu Gly Val Gly Val Ser Ser Thr Met Val Lys Asp Asn
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Asn Arg Ala Phe Asn Leu Pro Val Glu Asn Glu Lys Thr Glu Asp Tyr
 260 265 270

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Ser Arg Leu Pro Val Lys Asp Asn Ile Leu Lys Phe Asp Gln Ile Asn
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His Lys Ser Pro Thr Leu Ile Met Gly Ile Leu Asn Met Thr Pro Asp
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Ser Phe Ser Asp Gly Gly Lys His Phe Gly Lys Glu Leu Asp Asn Thr
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Val Lys Gln Ala Glu Lys Leu Val Ser Glu Gly Ala Thr Ile Ile Asp
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Ile Gly Gly Val Ser Thr Arg Pro Gly Ser Val Glu Pro Thr Glu Glu
 515 520 525

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Leu Asn Pro Asp Leu Leu Lys Val Leu Ile Ser Val Asp Thr Tyr Arg
 545 550 555 560

Arg Asn Val Ala Glu Gln Ser Leu Leu Val Gly Ala Asp Ile Ile Asn
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Asp Ile Ser Met Gly Lys Tyr Asp Glu Lys Ile Phe Asp Val Val Ala
 580 585 590

Lys Tyr Gly Cys Pro Tyr Ile Met Asn His Thr Arg Gly Ser Pro Lys
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Leu Gln Met Phe Lys Ala Met Ala Lys Gly Val Lys Lys Trp Gln Ile
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 690 695 700

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Thr Leu Thr Gly Asn Glu Val Pro Leu Asp Arg Val Phe Gly Thr Gly
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His Asp Val Lys Glu Met Lys Asp Val Val Cys Ile Ser Asp Ala Ile
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Tyr Lys Asn Val

785

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SEQUENCE LISTING

<110> Hoechst Marion Roussel

<120> ESSENTIAL GENES FROM C. ALBICANS AND A METHOD FOR
SCREENING ANTIMYCOTIC SUBSTANCES USING SAID GENES

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<170> PatentIn Ver. 2.1

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<223> Description of Artificial Sequence:probe

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SEQUENCE LISTING

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Ser	Leu	Phe	Lys	His	Val	Asp	Gly	Ala	Ser	Lys	Phe	Val	Gln	Pro	Leu		
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Pro	Thr	Thr	Gly	Gly	Ser	Asn	Gly	Gly	Ser	Lys	Ser	Arg	Leu	Gln	Ala		
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aga	tta	tta	gat	tca	aga	ctt	tca	tct	cct	tca	aat	aat	aat	gga	gat	1344	
Arg	Leu	Leu	Asp	Ser	Arg	Leu	Ser	Ser	Pro	Ser	Asn	Asn	Asn	Gly	Asp		
435								440				445					
tct	aaa	gaa	gag	aaa	cga	caa	tta	cgg	gaa	tca	tta	aga	aac	tca	ggc	1392	

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Ser	Lys	Glu	Glu	Lys	Arg	Gln	Leu	Arg	Glu	Ser	Leu	Arg	Asn	Ser	Gly	
450						455					460					
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Asn	Tyr	Lys	Glu	Gly	Val	Thr	Asp	Asp	Ala	Gly	Gly	Ala	Ala	Thr	Gly	
465					470					475					480	
ggg	ggg	agg	aaa	agt	gcc	ggg	act	cct	aat	aga	aat	agt	act	gat	tac	1488
Gly	Gly	Arg	Lys	Ser	Ala	Gly	Thr	Pro	Asn	Arg	Asn	Ser	Thr	Asp	Tyr	
				485					490					495		
gtt	tta	cat	gat	ata	tct	gct	cga	gta	cat	tca	cgt	aat	cga	tca	caa	1536
Val	Leu	His	Asp	Ile	Ser	Ala	Arg	Val	His	Ser	Arg	Asn	Arg	Ser	Gln	
			500					505					510			
gat	tta	ggg	aat	aat	ttc	aaa	tta	gct	aat	aat	ggg	aaa	tca	caa	ttt	1584
Asp	Leu	Gly	Asn	Asn	Phe	Lys	Leu	Ala	Asn	Asn	Gly	Lys	Ser	Gln	Phe	
			515				520					525				
ttc	aat	gaa	atc	aaa	act	tta	gaa	gat	cga	tta	gat	gat	gtt	gac	gtt	1632
Phe	Asn	Glu	Ile	Lys	Thr	Leu	Glu	Asp	Arg	Leu	Asp	Asp	Val	Asp	Val	
	530					535					540					
gaa	ata	tcg	cat	aat	caa	tat	gct	gaa	gcc	gtg	gaa	tta	ata	tca	ata	1680
Glu	Ile	Ser	His	Asn	Gln	Tyr	Ala	Glu	Ala	Val	Glu	Leu	Ile	Ser	Ile	
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Ile	Glu	Ser	Lys	Leu	Arg	Asn	Ile	Glu	Asn	Ala	Leu	Thr	Asn	Gln	Arg	
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Asn	Gly	Gly	Lys	Asn	Val	Asn	Ile	Ala	Asp	Glu	Leu	Leu	Leu	Leu	Asp	
			580					585					590			
gta	tca	aaa	ttg	aaa	att	aaa	aat	cgg	aaa	gaa	aat	gta	tct	aat	gga	1824
Val	Ser	Lys	Leu	Lys	Ile	Lys	Asn	Arg	Lys	Glu	Asn	Val	Ser	Asn	Gly	
			595				600					605				
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Leu	Ile	Phe	Asp	Leu	Gln	His	Asn	Ile	Ala	Lys	Leu	Lys	Gln	Asp	Asp	
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att	gat	aat	att	ttg	acg	tta	ttt	gat	aat	tta	gag	caa	tta	gat	cga	1920
Ile	Asp	Asn	Ile	Leu	Thr	Leu	Phe	Asp	Asn	Leu	Glu	Gln	Leu	Asp	Arg	
625					630					635					640	
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[illegible]

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Asn Asn Pro Tyr Ala Asn Leu Ser Thr Gly Glu Lys Ser Arg Ser Arg
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His Asn Thr Gly Ser Ser Tyr Val Ser Pro Tyr Gly Gly Gly Asn Gly
 50 55 60

Glu Glu Asn Ala Tyr Thr Gly Asn Asn Asn Lys Ser Asn Thr Ser Gly
 65 70 75 80

Asn Leu Leu Gln Val Pro Gly Ala Gly Gly Gly Gly Asp Leu Asn Ser
 85 90 95

Asn Lys Lys Gln Ser Arg Arg Met Ser Ile His Val Ser Ala Arg Gln
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His Gly Arg Ser Phe Ser Gln Thr Gly Pro Ile Asp Met Ala Asn Leu
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Pro Ala Leu Pro Lys Ile Gly Gly Val Thr Thr Ser Gly Val Gly Gly
 130 135 140

Ala Gly Gly Asp Val Met Thr Arg Thr Gly Gly Leu Thr Ile Glu Gln
 145 150 155 160

Lys Ile Phe Lys Glu Leu Ser Gln Gly Ser Ala Ala Glu Val Asp Asp
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Tyr Tyr Lys Thr Leu Leu Lys Gln Lys Asn Leu Ile Thr Arg Asp Ile
 180 185 190

Lys Asp Asn Ile Asn Gln Asn Gln Lys Asn Ile Leu Gln Leu Thr Lys
 195 200 205

Asp Leu Lys Glu Thr Gln Glu Glu Leu Ile Glu Leu Arg Gly Thr Thr
 210 215 220

Lys Glu Leu Tyr Glu Val Leu Gly Tyr Phe Lys Glu Ser Ala Gln Arg
 225 230 235 240

Arg Leu Glu Leu Glu Phe Glu Pro Glu Thr Gln Lys Glu Leu His Leu
 245 250 255

Pro Gln Lys Ser Asn Gln Leu Gly Ile Pro Ser Asn Lys Lys Lys Asp
 260 265 270

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Arg Ser Ser Ile Met Val Leu Lys Lys Met Trp Asp Ser Gln Leu Gln
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Ser Leu Phe Lys His Val Asp Gly Ala Ser Lys Phe Val Gln Pro Leu
 290 295 300

Pro Asn Arg His Ile Val Ala Glu Ser Gly Arg Trp Phe Glu Val Asn
 305 310 315 320

Val Gly Asn Trp Lys Pro Ser Tyr Pro Thr His Leu Phe Ile Phe Asn
 325 330 335

Asp Leu Ile Leu Ile Thr Val Lys Lys Ser Ser Ser Ser Ser Gln Glu
 340 345 350

Pro Thr Thr Gly Gly Ser Asn Gly Gly Ser Lys Ser Arg Leu Gln Ala
 355 360 365

Val Gln Cys Trp Pro Leu Thr Gln Val Ser Leu Gln Gln Ile Lys Ser
 370 375 380

Pro Lys Lys Asp Asp Asp Lys Met Tyr Phe Ile Asn Leu Lys Ser Lys
 385 390 395 400

Ser Leu Ser Tyr Val Tyr Leu Thr Asp Arg Tyr Asp His Phe Val Lys
 405 410 415

Val Thr Glu Ala Phe Asn Lys Gly Arg Asn Glu Met Ile Gln Ser Glu
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Arg Leu Leu Asp Ser Arg Leu Ser Ser Pro Ser Asn Asn Asn Gly Asp
 435 440 445

Ser Lys Glu Glu Lys Arg Gln Leu Arg Glu Ser Leu Arg Asn Ser Gly
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Asn Tyr Lys Glu Gly Val Thr Asp Asp Ala Gly Gly Ala Ala Thr Gly
 465 470 475 480

Gly Gly Arg Lys Ser Ala Gly Thr Pro Asn Arg Asn Ser Thr Asp Tyr
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Val Leu His Asp Ile Ser Ala Arg Val His Ser Arg Asn Arg Ser Gln
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Asp Leu Gly Asn Asn Phe Lys Leu Ala Asn Asn Gly Lys Ser Gln Phe
 515 520 525

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Phe Asn Glu Ile Lys Thr Leu Glu Asp Arg Leu Asp Asp Val Asp Val
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Glu Ile Ser His Asn Gln Tyr Ala Glu Ala Val Glu Leu Ile Ser Ile
 545 550 555 560

Ile Glu Ser Lys Leu Arg Asn Ile Glu Asn Ala Leu Thr Asn Gln Arg
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Asn Gly Gly Lys Asn Val Asn Ile Ala Asp Glu Leu Leu Leu Leu Asp
 580 585 590

Val Ser Lys Leu Lys Ile Lys Asn Arg Lys Glu Asn Val Ser Asn Gly
 595 600 605

Leu Ile Phe Asp Leu Gln His Asn Ile Ala Lys Leu Lys Gln Asp Asp
 610 615 620

Ile Asp Asn Ile Leu Thr Leu Phe Asp Asn Leu Glu Gln Leu Asp Arg
 625 630 635 640

Gly Val Gln Gly Tyr Leu Asp Ser Met Ser Ala Tyr Leu Ser Thr Thr
 645 650 655

Val Ser Lys Leu Ile Val Gly Leu Gln Gly Ser Thr Lys Ile Asp Val
 660 665 670

Val Asn Tyr Leu Ser Asn Leu Met Val Ile Asn Val Ser Ile Val Lys
 675 680 685

Arg Thr Ile Gln Thr Tyr Glu Gln Ile Ile Ala Pro Ile Leu Lys Arg
 690 695 700

His Gly Asp Val Asp Ser Ser Gly Leu Ile Asn Trp Cys Ile Asp Glu
 705 710 715 720

Phe Thr Lys Leu Cys Lys Gln Ile Lys Lys His Leu Tyr Gly Thr Leu
 725 730 735

Leu Ile Ser Ser Gly Ile Asn Met Glu Thr Asp Glu Pro Ile Tyr Lys
 740 745 750

Val Lys Glu Arg Lys Leu Tyr Asp Asn Phe Leu Lys Ile Met Gln Pro
 755 760 765

Gln Leu Glu Glu Leu Lys Leu Val Gly Leu Asn Val Asp Tyr Ile Phe
 770 775 780

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Glu Ser Ile Leu Asn Leu Glu
785 790

21/83

SEQUENCE LISTING

<110> Hoechst Marion Roussel

<120> ESSENTIAL GENES FROM C. ALBICANS AND A METHOD FOR
SCREENING ANTIMYCOTIC SUBSTANCES USING SAID GENES

<130> SEQID05

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<160> 1

<170> PatentIn Ver. 2.1

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<213> Artificial Sequence

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ccattggcaa tttaggatgt gaaaaaatag taaatatact atcggtatgt ttatcaaaat 180
aagtccatga attgttgga atgtcaattt cttaaagtctc atgctcatca tctaattcca 240
tctctcatc ttcttcatcg ggtggcgctt gatcatcatc tgcaacttcc tcagccactt 300
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SEQUENCE LISTING

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<120> ESSENTIAL GENES FROM C. ALBICANS AND A METHOD FOR
SCREENING ANTIMYCOTIC SUBSTANCES USING SAID GENES

<130> SEQID06

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<170> PatentIn Ver. 2.1

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<221> gene

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<223> gene CaIR012

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atc aat gtt aat gaa gtg gct gag gaa gtt gca gat gat gat caa gcg	96
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20 25 30	

cca ccc gat gaa gaa gat gag gag atg gaa tta gat gat gag cat gag	144
Pro Pro Asp Glu Glu Asp Glu Glu Met Glu Leu Asp Asp Glu His Glu	
35 40 45	

act tta gaa att gac atg tcc aac aat tca tgg act tat ttt gat aaa	192
Thr Leu Glu Ile Asp Met Ser Asn Asn Ser Trp Thr Tyr Phe Asp Lys	
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cat acc gat agt ata ttt act att ttt tca cat cct aaa ttg cca atg	240
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His	Thr	Asp	Ser	Ile	Phe	Thr	Ile	Phe	Ser	His	Pro	Lys	Leu	Pro	Met	
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gta	ttg	act	ggg	ggt	ggt	gac	aac	acg	gca	tac	tta	tgg	acc	aca	cac	288
Val	Leu	Thr	Gly	Gly	Gly	Asp	Asn	Thr	Ala	Tyr	Leu	Trp	Thr	Thr	His	
				85					90					95		
acc	caa	cca	cca	aga	ttt	gtt	ggc	gaa	atc	act	gga	cat	aaa	gag	tct	336
Thr	Gln	Pro	Pro	Arg	Phe	Val	Gly	Glu	Ile	Thr	Gly	His	Lys	Glu	Ser	
			100					105					110			
gtt	ata	tct	gga	ggg	ttt	act	gca	gac	ggc	aag	ttt	gtt	gtt	act	gca	384
Val	Ile	Ser	Gly	Gly	Phe	Thr	Ala	Asp	Gly	Lys	Phe	Val	Val	Thr	Ala	
		115					120					125				
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Asp	Met	Asn	Gly	Leu	Ile	Gln	Val	Phe	Lys	Ala	Thr	Lys	Gly	Gly	Glu	
	130					135					140					
cag	tgg	gtg	aaa	ttt	ggt	gaa	ttg	gac	gaa	gtt	gaa	gaa	gtg	ttg	ttt	480
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caa	att	atg	tct	ggg	ttc	tca	cac	aca	tta	gaa	tgt	aat	ggt	gct	gta	624
Gln	Ile	Met	Ser	Gly	Phe	Ser	His	Thr	Leu	Glu	Cys	Asn	Gly	Ala	Val	
		195					200					205				
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Phe	Ile	Gln	Gly	Lys	Asp	Glu	Asn	Asp	Leu	Thr	Leu	Val	Ser	Ile	Ser	
	210					215					220					
gaa	gat	ggt	act	gtg	gtg	aac	tgg	aac	tgt	ttt	aca	gga	caa	gtg	aat	720
Glu	Asp	Gly	Thr	Val	Val	Asn	Trp	Asn	Cys	Phe	Thr	Gly	Gln	Val	Asn	
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tat	aaa	ttg	caa	cct	cat	gat	gac	ttt	aaa	gga	gtt	gaa	agt	ccg	tgg	768
Tyr	Lys	Leu	Gln	Pro	His	Asp	Asp	Phe	Lys	Gly	Val	Glu	Ser	Pro	Trp	
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gtc	acg	gtc	aaa	gta	cat	ggt	aat	ctt	gtg	gcc	att	ggt	ggc	aga	gat	816

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Val Thr Val Lys Val His Gly Asn Leu Val Ala Ile Gly Gly Arg Asp
 260 265 270

ggc cag cta tca att gtg aac aat gac act ggt aaa atc gtt cat act 864
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 275 280 285

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 290 295 300

gca ttg agt tgg tgt gaa agc aaa aat att aac ctc ttg gca gtg ggt 960
 Ala Leu Ser Trp Cys Glu Ser Lys Asn Ile Asn Leu Leu Ala Val Gly
 305 310 315 320

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 325 330 335

aga aag aac ttg aaa gtt gac gat gcc atc acc aaa tta caa ttt gtt 1056
 Arg Lys Asn Leu Lys Val Asp Asp Ala Ile Thr Lys Leu Gln Phe Val
 340 345 350

ggc gaa acc ccc att ttg gtg gga agt agt atg gat ggt aaa att tac 1104
 Gly Glu Thr Pro Ile Leu Val Gly Ser Ser Met Asp Gly Lys Ile Tyr
 355 360 365

aaa tgg gac gct aga act ggt gaa gag ttg ttt gct ggt gtg gga cac 1152
 Lys Trp Asp Ala Arg Thr Gly Glu Glu Leu Phe Ala Gly Val Gly His
 370 375 380

aac atg gga gta ttg gac ttt gct att tta gat gga ggt aaa aag ttg 1200
 Asn Met Gly Val Leu Asp Phe Ala Ile Leu Asp Gly Gly Lys Lys Leu
 385 390 395 400

gtt act gct ggt gat gaa ggt gtt tca ttg gtc ttt gta cat gaa tag 1248
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<212> PRT

<213> Candida albicans

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Pro Pro Asp Glu Glu Asp Glu Glu Met Glu Leu Asp Asp Glu His Glu
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Thr Leu Glu Ile Asp Met Ser Asn Asn Ser Trp Thr Tyr Phe Asp Lys
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His Thr Asp Ser Ile Phe Thr Ile Phe Ser His Pro Lys Leu Pro Met
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 115 120 125

Asp Met Asn Gly Leu Ile Gln Val Phe Lys Ala Thr Lys Gly Gly Glu
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Gln Trp Val Lys Phe Gly Glu Leu Asp Glu Val Glu Glu Val Leu Phe
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Val Thr Val His Pro Thr Leu Pro Phe Phe Ala Phe Gly Ala Thr Asp
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Gly Ser Ile Trp Val Tyr Gln Ile Asp Glu Ser Ser Lys Leu Leu Val
 180 185 190

Gln Ile Met Ser Gly Phe Ser His Thr Leu Glu Cys Asn Gly Ala Val
 195 200 205

Phe Ile Gln Gly Lys Asp Glu Asn Asp Leu Thr Leu Val Ser Ile Ser
 210 215 220

Glu Asp Gly Thr Val Val Asn Trp Asn Cys Phe Thr Gly Gln Val Asn
 225 230 235 240

Tyr Lys Leu Gln Pro His Asp Asp Phe Lys Gly Val Glu Ser Pro Trp
 245 250 255

Val Thr Val Lys Val His Gly Asn Leu Val Ala Ile Gly Gly Arg Asp
 260 265 270

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Gly Gln Leu Ser Ile Val Asn Asn Asp Thr Gly Lys Ile Val His Thr
 275 280 285

Leu Lys Thr Leu Asp Asn Val Asp Asp Ile Ala Glu Leu Ser Ile Glu
 290 295 300

Ala Leu Ser Trp Cys Glu Ser Lys Asn Ile Asn Leu Leu Ala Val Gly
 305 310 315 320

Leu Val Ser Gly Asp Val Leu Leu Phe Asp Thr Gln Gln Trp Arg Leu
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Arg Lys Asn Leu Lys Val Asp Asp Ala Ile Thr Lys Leu Gln Phe Val
 340 345 350

Gly Glu Thr Pro Ile Leu Val Gly Ser Ser Met Asp Gly Lys Ile Tyr
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Lys Trp Asp Ala Arg Thr Gly Glu Glu Leu Phe Ala Gly Val Gly His
 370 375 380

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SEQUENCE LISTING

<110> Hoechst Marion Roussel

<120> ESSENTIAL GENES FROM C. ALBICANS AND A METHOD FOR
SCREENING ANTIMYCOTIC SUBSTANCES USING SAID GENES

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<170> PatentIn Ver. 2.1

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<211> 5544

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<213> Candida albicans

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aac acc ctc aag ttt gag tcc aat ata gat ttg gat aca atc gac ttc	96
Asn Thr Leu Lys Phe Glu Ser Asn Ile Asp Leu Asp Thr Ile Asp Phe	
20 25 30	

acc agc atc aag aat gat ctt gca aat gtt ttg att aca cca gtc cct	144
Thr Ser Ile Lys Asn Asp Leu Ala Asn Val Leu Ile Thr Pro Val Pro	
35 40 45	

ctg gat caa tca cgt agc aaa ctt gga gac gca tca aaa cca gtg gcg	192
Leu Asp Gln Ser Arg Ser Lys Leu Gly Asp Ala Ser Lys Pro Val Ala	
50 55 60	

ttg ccc agt gga gat gag gtg aaa ttg aat caa gca tca att gaa att	240
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 260 265 270

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 275 280 285

aaa agt gaa gat att gac ttg tca aaa tca aaa ttg tct ggc ttt gaa 912
 Lys Ser Glu Asp Ile Asp Leu Ser Lys Ser Lys Leu Ser Gly Phe Glu
 290 295 300

ata gtc aca agc ttt att ttt cta act gag ttt att cca tgg tgc aag 960
 Ile Val Thr Ser Phe Ile Phe Leu Thr Glu Phe Ile Pro Trp Cys Lys
 305 310 315 320

cag ctg tca agt aga acc gcg aaa tac gat ttc aaa gat gat ata tta 1008
 Gln Leu Ser Ser Arg Thr Ala Lys Tyr Asp Phe Lys Asp Asp Ile Leu
 325 330 335

aag tat atg gaa ttc ttg ata agt tat gga gtt atg gaa cga tta tta 1056
 Lys Tyr Met Glu Phe Leu Ile Ser Tyr Gly Val Met Glu Arg Leu Leu
 340 345 350

tca tac tgt tct gaa acc agc aat gca aaa act cag caa gtg tac gac 1104
 Ser Tyr Cys Ser Glu Thr Ser Asn Ala Lys Thr Gln Gln Val Tyr Asp
 355 360 365

tgg tca aac atg tac gat ttc aga gca ttg ctt caa aag aat ttc cca 1152
 Trp Ser Asn Met Tyr Asp Phe Arg Ala Leu Leu Gln Lys Asn Phe Pro
 370 375 380

cga ctt aca cca gca aaa ttt cat tat cct ggc aat caa gaa ttg ttg 1200
 Arg Leu Thr Pro Ala Lys Phe His Tyr Pro Gly Asn Gln Glu Leu Leu
 385 390 395 400

aat gca gtt aga ccg gga tat gaa aat ata tcc aaa ttg att gac att 1248
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 405 410 415

tcc ttt ttg acg tta gat cca tcg ctt aat gag acg ttg gtt tca cct 1296
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 420 425 430

ttt ttc cag agc ttt ttc agt gtg ttt ata tct aat gcc gca gtt gtt 1344
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atg acc tct tta agg gac tca gag gaa gat ttt gtt tta tcg tcg ttg 1392

30/83

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Asn	Glu	Ser	Asp	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Ser	Asp	Ser	Asp	Glu	
465					470					475					480	
gat	tct	tcg	acc	cca	aaa	aac	aaa	gaa	aaa	tca	gct	ggg	tta	gac	ctt	1488
Asp	Ser	Ser	Thr	Pro	Lys	Asn	Lys	Glu	Lys	Ser	Ala	Gly	Leu	Asp	Leu	
				485					490					495		
gac	aag	att	gcc	cag	cgt	gct	gaa	tta	gaa	agg	ttc	tac	ttg	gct	ttc	1536
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			500					505					510			
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		515				520					525					
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Asn	Glu	Gln	Val	Thr	His	Asp	Ile	Ile	Gly	Phe	Ile	Ser	Trp	Gly	Leu	
	530					535				540						
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Ala	Asn	Asn	Thr	Ser	Pro	Leu	Ile	Thr	Ala	Thr	Phe	Cys	Leu	Leu	Leu	
545					550					555					560	
ggg	tcg	ttg	gca	tct	gct	ggt	gca	gag	gca	act	tca	agg	ata	tgg	gag	1728
Gly	Ser	Leu	Ala	Ser	Ala	Gly	Ala	Glu	Ala	Thr	Ser	Arg	Ile	Trp	Glu	
			565					570					575			
att	ctt	gta	cac	aac	aat	aac	aac	gca	agt	acg	aga	aaa	aat	gat	ttt	1776
Ile	Leu	Val	His	Asn	Asn	Asn	Asn	Ala	Ser	Thr	Arg	Lys	Asn	Asp	Phe	
		580						585					590			
tca	aag	gta	tcc	gtt	gac	tcc	ctt	tat	gat	tcg	ttg	aaa	tat	tac	att	1824
Ser	Lys	Val	Ser	Val	Asp	Ser	Leu	Tyr	Asp	Ser	Leu	Lys	Tyr	Tyr	Ile	
		595					600					605				
gac	tct	tta	aat	gaa	agc	ttt	gaa	caa	gat	tta	aat	gcc	caa	ttg	atg	1872
Asp	Ser	Leu	Asn	Glu	Ser	Phe	Glu	Gln	Asp	Leu	Asn	Ala	Gln	Leu	Met	
	610					615						620				
ttg	aat	cag	aag	aaa	caa	gat	ttt	ctc	ttc	agc	acc	aca	aca	agc	aaa	1920
Leu	Asn	Gln	Lys	Lys	Gln	Asp	Phe	Leu	Phe	Ser	Thr	Thr	Thr	Ser	Lys	
625					630					635					640	
cag	gac	ctt	gat	gat	tct	ggc	gag	aat	aga	att	gtt	ata	gag	ttg	gcc	1968

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Gln Asp Leu Asp Asp Ser Gly Glu Asn Arg Ile Val Ile Glu Leu Ala	
645 650 655	
gag gat tca ctt gtc ctc att tca ggg ttt att caa tta ctt tct gca	2016
Glu Asp Ser Leu Val Leu Ile Ser Gly Phe Ile Gln Leu Leu Ser Ala	
660 665 670	
att gtg aag aat ttg aac act aag aat gaa aga agc aaa gaa atc aaa	2064
Ile Val Lys Asn Leu Asn Thr Lys Asn Glu Arg Ser Lys Glu Ile Lys	
675 680 685	
tcc gtg gta tac act aga ttc tca cca atc att aaa ggg ttt tta aaa	2112
Ser Val Val Tyr Thr Arg Phe Ser Pro Ile Ile Lys Gly Phe Leu Lys	
690 695 700	
ttc gat aat ttg atc aat ggt agc agg ttc ctt caa gtt gat gct agc	2160
Phe Asp Asn Leu Ile Asn Gly Ser Arg Phe Leu Gln Val Asp Ala Ser	
705 710 715 720	
att caa agc aca aac aac ccc aaa ttt att gat ttg cca aat gtt ttc	2208
Ile Gln Ser Thr Asn Asn Pro Lys Phe Ile Asp Leu Pro Asn Val Phe	
725 730 735	
gtc agt gat gac tcg aga att ata ttg acg aac ctc att cta acc ttt	2256
Val Ser Asp Asp Ser Arg Ile Ile Leu Thr Asn Leu Ile Leu Thr Phe	
740 745 750	
tta ggc gat ttt gtt acc aac gat agt gat ccg tat att aga tat gag	2304
Leu Gly Asp Phe Val Thr Asn Asp Ser Asp Pro Tyr Ile Arg Tyr Glu	
755 760 765	
att tgg cgt tta gtc gat cga tgg atg tac cag ggg ttg cat agt ttg	2352
Ile Trp Arg Leu Val Asp Arg Trp Met Tyr Gln Gly Leu His Ser Leu	
770 775 780	
cca gaa gac aag aaa gat gat gct ttt aga cat att aag aga aag tat	2400
Pro Glu Asp Lys Lys Asp Asp Ala Phe Arg His Ile Lys Arg Lys Tyr	
785 790 795 800	
aac agt aag aaa aat gtt ccc atc aat caa gca ttt tca aca aac cta	2448
Asn Ser Lys Lys Asn Val Pro Ile Asn Gln Ala Phe Ser Thr Asn Leu	
805 810 815	
act cat ctt agt caa att ggg aat ttc act gtc ttg gtg aaa aaa ttg	2496
Thr His Leu Ser Gln Ile Gly Asn Phe Thr Val Leu Val Lys Lys Leu	
820 825 830	
tta acc cca tat gca gat agt aat gaa gca ttc acc aag tac tcg ttg	2544

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Leu Thr Pro Tyr Ala Asp Ser Asn Glu Ala Phe Thr Lys Tyr Ser Leu	
835 840 845	
ttg tat cct tgt gac tta gga tta ggg tat aga ttc aac aac caa ctt	2592
Leu Tyr Pro Cys Asp Leu Gly Leu Gly Tyr Arg Phe Asn Asn Gln Leu	
850 855 860	
gga att tgg cca tac att gaa ttt tta atg caa aat gtg ttt gca aat	2640
Gly Ile Trp Pro Tyr Ile Glu Phe Leu Met Gln Asn Val Phe Ala Asn	
865 870 875 880	
tct ggt act att gct aat aaa cga gat agg gtc aac ttg caa ctt aat	2688
Ser Gly Thr Ile Ala Asn Lys Arg Asp Arg Val Asn Leu Gln Leu Asn	
885 890 895	
ttg cta gaa tta ttt agc aat gca tta cag gga gtt gac tgg aag ttt	2736
Leu Leu Glu Leu Phe Ser Asn Ala Leu Gln Gly Val Asp Trp Lys Phe	
900 905 910	
ctt att gat gtg gca ccg aaa att att cgt gac ttg aaa aat ttt aat	2784
Leu Ile Asp Val Ala Pro Lys Ile Ile Arg Asp Leu Lys Asn Phe Asn	
915 920 925	
ggg ata ttt gac tcg ctt att cct ggt gtt caa ttg gac ttt gaa gtg	2832
Gly Ile Phe Asp Ser Leu Ile Pro Gly Val Gln Leu Asp Phe Glu Val	
930 935 940	
ttt gtc aaa ttg cat cat tca gtt gct gtg att aac tat cta ttt gaa	2880
Phe Val Lys Leu His His Ser Val Ala Val Ile Asn Tyr Leu Phe Glu	
945 950 955 960	
aac agg aca ttt tct gcc ttg ttt aag ctt gtt aat att gga gtt gat	2928
Asn Arg Thr Phe Ser Ala Leu Phe Lys Leu Val Asn Ile Gly Val Asp	
965 970 975	
tct gtg aat gaa tca ggt gaa tcg gcg gaa ttg gtg tca cat gcc ctt	2976
Ser Val Asn Glu Ser Gly Glu Ser Ala Glu Leu Val Ser His Ala Leu	
980 985 990	
ggg ttg att aat tct ttg ttg aga gtt caa aat tct ttt ata aac aag	3024
Gly Leu Ile Asn Ser Leu Leu Arg Val Gln Asn Ser Phe Ile Asn Lys	
995 1000 1005	
ttg tta cca ata ttg cga aac aaa gat acg cag caa caa tta cat cgt	3072
Leu Leu Pro Ile Leu Arg Asn Lys Asp Thr Gln Gln Gln Leu His Arg	
1010 1015 1020	
ggg aca gcc att ggg att ggt act tct atg agt ctt gcg tta gca acc	3120

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Gly Thr Ala Ile Gly Ile Gly Thr Ser Met Ser Leu Ala Leu Ala Thr	1025	1030	1035	1040
cct aga acc ata ttt gat tgt ata tac tat cca aag aat ttg gga aca				3168
Pro Arg Thr Ile Phe Asp Cys Ile Tyr Tyr Pro Lys Asn Leu Gly Thr	1045	1050	1055	
cat ggt gtt gct gat ttt tac gaa gtg ata ttg ttc cac tta tct gca				3216
His Gly Val Ala Asp Phe Tyr Glu Val Ile Leu Phe His Leu Ser Ala	1060	1065	1070	
gtt gtc caa ttt gcc ctt tat gtc agt tgt gaa aat act att tcc aac				3264
Val Val Gln Phe Ala Leu Tyr Val Ser Cys Glu Asn Thr Ile Ser Asn	1075	1080	1085	
aaa gca att tcc ata ttg aaa gga gta agc caa tcc aag ttt ttt gtt				3312
Lys Ala Ile Ser Ile Leu Lys Gly Val Ser Gln Ser Lys Phe Phe Val	1090	1095	1100	
acc aga gtt tca agc tct gct gat ccc tta ctc aac aac gat aga ttg				3360
Thr Arg Val Ser Ser Ser Ala Asp Pro Leu Leu Asn Asn Asp Arg Leu	1105	1110	1115	1120
att acc aca ttt gaa aac atc gac gag tca ata aaa atc aag ttt gct				3408
Ile Thr Thr Phe Glu Asn Ile Asp Glu Ser Ile Lys Ile Lys Phe Ala	1125	1130	1135	
ttc att gac aag ttt gaa gaa ctc gag gac tct ttg aat atg aaa tat				3456
Phe Ile Asp Lys Phe Glu Glu Leu Glu Asp Ser Leu Asn Met Lys Tyr	1140	1145	1150	
gag ata ttg gat ttt gtt ttg ggc aat ctc aat caa ttt gat ggc aaa				3504
Glu Ile Leu Asp Phe Val Leu Gly Asn Leu Asn Gln Phe Asp Gly Lys	1155	1160	1165	
gtg gct act act gcc cac ttt ttg ttg gga tac aaa gtg aaa ggc gat				3552
Val Ala Thr Thr Ala His Phe Leu Leu Gly Tyr Lys Val Lys Gly Asp	1170	1175	1180	
aca tta gac ttg gta cag aca aac gat caa aac aca tta cta aaa tct				3600
Thr Leu Asp Leu Val Gln Thr Asn Asp Gln Asn Thr Leu Leu Lys Ser	1185	1190	1195	1200
ttc tta aat aca ttg agc att agt ctt gat ttg att tct gaa att gat				3648
Phe Leu Asn Thr Leu Ser Ile Ser Leu Asp Leu Ile Ser Glu Ile Asp	1205	1210	1215	
tac aat aat ggt aat aac cat att att gat gtt ggt cca gcc aag ctt				3696

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Tyr Asn Asn Gly Asn Asn His Ile Ile Asp Val Gly Pro Ala Lys Leu	
1220	1225 1230
tcg tcg ttg att tta cag att ctt atc aag ttg tgc caa gat cca att	3744
Ser Ser Leu Ile Leu Gln Ile Leu Ile Lys Leu Cys Gln Asp Pro Ile	
1235	1240 1245
tcg tcg tca ata aca ttg aat caa tta cgt gaa tat gaa gaa ttg ttt	3792
Ser Ser Ser Ile Thr Leu Asn Gln Leu Arg Glu Tyr Glu Glu Leu Phe	
1250	1255 1260
gaa aaa ttg gtt aac tgt caa cct aaa ctt gat ttg aat acc gtt tgg	3840
Glu Lys Leu Val Asn Cys Gln Pro Lys Leu Asp Leu Asn Thr Val Trp	
1265	1270 1275 1280
tgt ggt aac cag ttt gat ggg gat ttg cag att gat gct agc aat gta	3888
Cys Gly Asn Gln Phe Asp Gly Asp Leu Gln Ile Asp Ala Ser Asn Val	
1285	1290 1295
ttt gtt gac aac caa gca agc acc cag gct ttc ttt tcc ttt att aac	3936
Phe Val Asp Asn Gln Ala Ser Thr Gln Ala Phe Phe Ser Phe Ile Asn	
1300	1305 1310
cag aga aac tta att ttg cag tat ttg tca ttg gaa ttc cat agt gtc	3984
Gln Arg Asn Leu Ile Leu Gln Tyr Leu Ser Leu Glu Phe His Ser Val	
1315	1320 1325
aaa tca aga act aag cgg gag tat tat tct aaa gtg ttg acc aac gac	4032
Lys Ser Arg Thr Lys Arg Glu Tyr Tyr Ser Lys Val Leu Thr Asn Asp	
1330	1335 1340
aag gaa ttt gtt aat cgt aca cct aag gtg ttg aca ttt tta aac att	4080
Lys Glu Phe Val Asn Arg Thr Pro Lys Val Leu Thr Phe Leu Asn Ile	
1345	1350 1355 1360
cta aat tat tca ttc aag aac ttt gaa gtg cag aaa tac gaa tgg ctt	4128
Leu Asn Tyr Ser Phe Lys Asn Phe Glu Val Gln Lys Tyr Glu Trp Leu	
1365	1370 1375
gac caa aaa ttt aac gtg tcg ttg tta ttg gca gaa gta aac gct caa	4176
Asp Gln Lys Phe Asn Val Ser Leu Leu Leu Ala Glu Val Asn Ala Gln	
1380	1385 1390
aag aat ggt aca tta gat ttt tct gtt tta aca aag gtt ttc cgt ctt	4224
Lys Asn Gly Thr Leu Asp Phe Ser Val Leu Thr Lys Val Phe Arg Leu	
1395	1400 1405
ttg tgc caa acg tca aac tta ata aca ccc gag tca aag caa ttg ttt	4272

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Leu Cys Gln Thr Ser Asn Leu Ile Thr Pro Glu Ser Lys Gln Leu Phe
 1410 1415 1420

gcc gaa gaa att atg gtt gaa gga agt aag att tct gac ttt gtc aca 4320
 Ala Glu Glu Ile Met Val Glu Gly Ser Lys Ile Ser Asp Phe Val Thr
 1425 1430 1435 1440

aag tac ctg gtg tct acc gac ttg aag gat gtg cag ttg aaa tgc tta 4368
 Lys Tyr Leu Val Ser Thr Asp Leu Lys Asp Val Gln Leu Lys Cys Leu
 1445 1450 1455

cat tca tgg tgt caa ttg ata gag att ttg gtt act gac agt gga atc 4416
 His Ser Trp Cys Gln Leu Ile Glu Ile Leu Val Thr Asp Ser Gly Ile
 1460 1465 1470

aat tct ctg aat ttc atc ttg gaa gtg ttg caa gtt att att ccc aaa 4464
 Asn Ser Leu Asn Phe Ile Leu Glu Val Leu Gln Val Ile Ile Pro Lys
 1475 1480 1485

atc aat gac tat ttt gat gtg gac ata ctg ttt tct gaa gaa atg gtt 4512
 Ile Asn Asp Tyr Phe Asp Val Asp Ile Leu Phe Ser Glu Glu Met Val
 1490 1495 1500

tca tta tgt gtt tta ttg ttt gat ctt tat gat cag ctg act ctt gcg 4560
 Ser Leu Cys Val Leu Leu Phe Asp Leu Tyr Asp Gln Leu Thr Leu Ala
 1505 1510 1515 1520

gac aga aaa ggt gaa gat ttt gca ctt gga att gag aga ttg atc ccc 4608
 Asp Arg Lys Gly Glu Asp Phe Ala Leu Gly Ile Glu Arg Leu Ile Pro
 1525 1530 1535

tta ttt cag act tgt att gca ggt att ctt aat tct aac tca aca ccc 4656
 Leu Phe Gln Thr Cys Ile Ala Gly Ile Leu Asn Ser Asn Ser Thr Pro
 1540 1545 1550

agc tta cgc tca gac ttg tat gta gtt ggc aac aag ttt ttg tta aaa 4704
 Ser Leu Arg Ser Asp Leu Tyr Val Val Gly Asn Lys Phe Leu Leu Lys
 1555 1560 1565

tgt ttt gag aga gag tct ttt ttg aaa caa gtg atg cat atc atc aag 4752
 Cys Phe Glu Arg Glu Ser Phe Leu Lys Gln Val Met His Ile Ile Lys
 1570 1575 1580

tct gta gat aaa aag ttt ttc cag gtg att tgt aat gac gct atc tac 4800
 Ser Val Asp Lys Lys Phe Phe Gln Val Ile Cys Asn Asp Ala Ile Tyr
 1585 1590 1595 1600

tca gag ggt cca tct aga atc act tct act tta ttc ctc gag tca tta 4848

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Ser Glu Gly Pro Ser Arg Ile Thr Ser Thr Leu Phe Leu Glu Ser Leu	
1605 1610 1615	
ggt cac tta ggg act ttg gtc aag gtt gat ttt att ttg aat gcg ttg	4896
Val His Leu Gly Thr Leu Val Lys Val Asp Phe Ile Leu Asn Ala Leu	
1620 1625 1630	
atc aaa aat aac gca ttg ctg ttg cta gtc agg tca gtt aag cgg act	4944
Ile Lys Asn Asn Ala Leu Leu Leu Leu Val Arg Ser Val Lys Arg Thr	
1635 1640 1645	
gat gcc atg atc aaa ttg tgc cag gaa aaa aat tca gga gtg act tta	4992
Asp Ala Met Ile Lys Leu Cys Gln Glu Lys Asn Ser Gly Val Thr Leu	
1650 1655 1660	
gat cat ttc ata ttt gac ttg atg gca ttc aaa gca acg cta tat ttt	5040
Asp His Phe Ile Phe Asp Leu Met Ala Phe Lys Ala Thr Leu Tyr Phe	
1665 1670 1675 1680	
ttt gtt aga gtg gcc aaa tcg aaa aac ggg gca ttg cag ttg att caa	5088
Phe Val Arg Val Ala Lys Ser Lys Asn Gly Ala Leu Gln Leu Ile Gln	
1685 1690 1695	
aat gaa ttg ttt tca att ttg cat cag tcg aag ttt ttg cag att gat	5136
Asn Glu Leu Phe Ser Ile Leu His Gln Ser Lys Phe Leu Gln Ile Asp	
1700 1705 1710	
cca gat att ggt tta agt tta cga att gaa gaa gtt caa gat cac aag	5184
Pro Asp Ile Gly Leu Ser Leu Arg Ile Glu Glu Val Gln Asp His Lys	
1715 1720 1725	
act gtc aat gta aat gtt ttg cta gat act cca ctt tcg ata act gac	5232
Thr Val Asn Val Asn Val Leu Leu Asp Thr Pro Leu Ser Ile Thr Asp	
1730 1735 1740	
ttg gtg gat cca tac aag ttg cga agt gaa aac act ata tca tat ttt	5280
Leu Val Asp Pro Tyr Lys Leu Arg Ser Glu Asn Thr Ile Ser Tyr Phe	
1745 1750 1755 1760	
gag ttc ctt gta cca ata ttt cag cta ctt aca aca gtg tta ttg tca	5328
Glu Phe Leu Val Pro Ile Phe Gln Leu Leu Thr Thr Val Leu Leu Ser	
1765 1770 1775	
atg gga cca aat tat caa cct gca att att caa act aga gaa ctt atg	5376
Met Gly Pro Asn Tyr Gln Pro Ala Ile Ile Gln Thr Arg Glu Leu Met	
1780 1785 1790	
aag agt gta aat cga ttg gtg gta ggt gtt atg aaa aga gat ttc ttg	5424

37183

Lys Ser Val Asn Arg Leu Val Val Gly Val Met Lys Arg Asp Phe Leu
 1795 1800 1805

gta gag acc aaa caa att ggt caa ggg ttg tac aag gaa gag agt cac 5472
 Val Glu Thr Lys Gln Ile Gly Gln Gly Leu Tyr Lys Glu Glu Ser His
 1810 1815 1820

gag ttg gta tcg ttg aaa gaa ttg gtg aag ttg ttt att ttg att gat 5520
 Glu Leu Val Ser Leu Lys Glu Leu Val Lys Leu Phe Ile Leu Ile Asp
 1825 1830 1835 1840

tca tta gct cat tat agt gtg tag 5544
 Ser Leu Ala His Tyr Ser Val
 1845

<210> 2

<211> 1847

<212> PRT

<213> Candida albicans

<400> 2

Met Ser Gly Ile Phe Asn Trp Ser Leu Asp Val Phe Ala Asp Ile Tyr
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Asn Thr Leu Lys Phe Glu Ser Asn Ile Asp Leu Asp Thr Ile Asp Phe
 20 25 30

Thr Ser Ile Lys Asn Asp Leu Ala Asn Val Leu Ile Thr Pro Val Pro
 35 40 45

Leu Asp Gln Ser Arg Ser Lys Leu Gly Asp Ala Ser Lys Pro Val Ala
 50 55 60

Leu Pro Ser Gly Asp Glu Val Lys Leu Asn Gln Ala Ser Ile Glu Ile
 65 70 75 80

Thr Gly Val Leu Ser Asn Glu Leu Asp Leu Asp Glu Leu Asn Thr Ala
 85 90 95

Glu Leu Leu Tyr Asn Ala Ser Asp Leu Ser Tyr Lys Lys Gly Thr Ser
 100 105 110

Ile Gly Asp Ser Ala Arg Leu Ala Tyr Tyr Leu Arg Ala His Tyr Ile
 115 120 125

Leu Asn Ile Val Gly Tyr Leu Val Ser His Lys Arg Leu Asp Ile Ile
 130 135 140

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Thr Asn Asn Asn Gln Val Leu Phe Asp Asn Ile Leu Lys Ser Phe Ser
 145 150 155 160

Lys Ile Tyr Thr Leu Ser Gly Lys Leu Asn Asp Met Ile Asp Lys Gln
 165 170 175

Lys Val Thr Gly Asp Ile Asn Asn Leu Ala Phe Ile Asn Cys Ile Asn
 180 185 190

Tyr Ser Arg Ser Gln Leu Phe Asn Ala His Glu Leu Leu Gly Gln Val
 195 200 205

Val Phe Gly Leu Ala Asp Asn Tyr Tyr Glu Ser Tyr Gly Thr Leu Asn
 210 215 220

Asn Tyr Asn Ser Leu Val Glu Phe Ile Leu Lys Asn Ile Ser Asp Glu
 225 230 235 240

Asp Val Phe Val Ile His Phe Leu Pro Ser Thr Leu Gln Leu Phe Lys
 245 250 255

Lys Leu Leu Gln Leu Gly Glu Glu Ser Leu Val Asp Gln Phe Tyr Lys
 260 265 270

Thr Ile Thr Ser Ser Ile Leu Lys Asp Tyr Glu Ala Asn Asn Phe Ser
 275 280 285

Lys Ser Glu Asp Ile Asp Leu Ser Lys Ser Lys Leu Ser Gly Phe Glu
 290 295 300

Ile Val Thr Ser Phe Ile Phe Leu Thr Glu Phe Ile Pro Trp Cys Lys
 305 310 315 320

Gln Leu Ser Ser Arg Thr Ala Lys Tyr Asp Phe Lys Asp Asp Ile Leu
 325 330 335

Lys Tyr Met Glu Phe Leu Ile Ser Tyr Gly Val Met Glu Arg Leu Leu
 340 345 350

Ser Tyr Cys Ser Glu Thr Ser Asn Ala Lys Thr Gln Gln Val Tyr Asp
 355 360 365

Trp Ser Asn Met Tyr Asp Phe Arg Ala Leu Leu Gln Lys Asn Phe Pro
 370 375 380

Arg Leu Thr Pro Ala Lys Phe His Tyr Pro Gly Asn Gln Glu Leu Leu
 385 390 395 400

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Asn Ala Val Arg Pro Gly Tyr Glu Asn Ile Ser Lys Leu Ile Asp Ile
 405 410 415

Ser Phe Leu Thr Leu Asp Pro Ser Leu Asn Glu Thr Leu Val Ser Pro
 420 425 430

Phe Phe Gln Ser Phe Phe Ser Val Phe Ile Ser Asn Ala Ala Val Val
 435 440 445

Met Thr Ser Leu Arg Asp Ser Glu Glu Asp Phe Val Leu Ser Ser Leu
 450 455 460

Asn Glu Ser Asp Glu Glu Glu Glu Glu Glu Ser Asp Ser Asp Glu
 465 470 475 480

Asp Ser Ser Thr Pro Lys Asn Lys Glu Lys Ser Ala Gly Leu Asp Leu
 485 490 495

Asp Lys Ile Ala Gln Arg Ala Glu Leu Glu Arg Phe Tyr Leu Ala Phe
 500 505 510

Ala Tyr Thr Tyr Asn Asn Arg Pro Glu Leu Cys Ala Leu Phe Trp Gly
 515 520 525

Asn Glu Gln Val Thr His Asp Ile Ile Gly Phe Ile Ser Trp Gly Leu
 530 535 540

Ala Asn Asn Thr Ser Pro Leu Ile Thr Ala Thr Phe Cys Leu Leu Leu
 545 550 555 560

Gly Ser Leu Ala Ser Ala Gly Ala Glu Ala Thr Ser Arg Ile Trp Glu
 565 570 575

Ile Leu Val His Asn Asn Asn Asn Ala Ser Thr Arg Lys Asn Asp Phe
 580 585 590

Ser Lys Val Ser Val Asp Ser Leu Tyr Asp Ser Leu Lys Tyr Tyr Ile
 595 600 605

Asp Ser Leu Asn Glu Ser Phe Glu Gln Asp Leu Asn Ala Gln Leu Met
 610 615 620

Leu Asn Gln Lys Lys Gln Asp Phe Leu Phe Ser Thr Thr Thr Ser Lys
 625 630 635 640

Gln Asp Leu Asp Asp Ser Gly Glu Asn Arg Ile Val Ile Glu Leu Ala
 645 650 655

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Glu Asp Ser Leu Val Leu Ile Ser Gly Phe Ile Gln Leu Leu Ser Ala
 660 665 670

Ile Val Lys Asn Leu Asn Thr Lys Asn Glu Arg Ser Lys Glu Ile Lys
 675 680 685

Ser Val Val Tyr Thr Arg Phe Ser Pro Ile Ile Lys Gly Phe Leu Lys
 690 695 700

Phe Asp Asn Leu Ile Asn Gly Ser Arg Phe Leu Gln Val Asp Ala Ser
 705 710 715 720

Ile Gln Ser Thr Asn Asn Pro Lys Phe Ile Asp Leu Pro Asn Val Phe
 725 730 735

Val Ser Asp Asp Ser Arg Ile Ile Leu Thr Asn Leu Ile Leu Thr Phe
 740 745 750

Leu Gly Asp Phe Val Thr Asn Asp Ser Asp Pro Tyr Ile Arg Tyr Glu
 755 760 765

Ile Trp Arg Leu Val Asp Arg Trp Met Tyr Gln Gly Leu His Ser Leu
 770 775 780

Pro Glu Asp Lys Lys Asp Asp Ala Phe Arg His Ile Lys Arg Lys Tyr
 785 790 795 800

Asn Ser Lys Lys Asn Val Pro Ile Asn Gln Ala Phe Ser Thr Asn Leu
 805 810 815

Thr His Leu Ser Gln Ile Gly Asn Phe Thr Val Leu Val Lys Lys Leu
 820 825 830

Leu Thr Pro Tyr Ala Asp Ser Asn Glu Ala Phe Thr Lys Tyr Ser Leu
 835 840 845

Leu Tyr Pro Cys Asp Leu Gly Leu Gly Tyr Arg Phe Asn Asn Gln Leu
 850 855 860

Gly Ile Trp Pro Tyr Ile Glu Phe Leu Met Gln Asn Val Phe Ala Asn
 865 870 875 880

Ser Gly Thr Ile Ala Asn Lys Arg Asp Arg Val Asn Leu Gln Leu Asn
 885 890 895

Leu Leu Glu Leu Phe Ser Asn Ala Leu Gln Gly Val Asp Trp Lys Phe
 900 905 910

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Leu Ile Asp Val Ala Pro Lys Ile Ile Arg Asp Leu Lys Asn Phe Asn
 915 920 925

Gly Ile Phe Asp Ser Leu Ile Pro Gly Val Gln Leu Asp Phe Glu Val
 930 935 940

Phe Val Lys Leu His His Ser Val Ala Val Ile Asn Tyr Leu Phe Glu
 945 950 955 960

Asn Arg Thr Phe Ser Ala Leu Phe Lys Leu Val Asn Ile Gly Val Asp
 965 970 975

Ser Val Asn Glu Ser Gly Glu Ser Ala Glu Leu Val Ser His Ala Leu
 980 985 990

Gly Leu Ile Asn Ser Leu Leu Arg Val Gln Asn Ser Phe Ile Asn Lys
 995 1000 1005

Leu Leu Pro Ile Leu Arg Asn Lys Asp Thr Gln Gln Gln Leu His Arg
 1010 1015 1020

Gly Thr Ala Ile Gly Ile Gly Thr Ser Met Ser Leu Ala Leu Ala Thr
 1025 1030 1035 1040

Pro Arg Thr Ile Phe Asp Cys Ile Tyr Tyr Pro Lys Asn Leu Gly Thr
 1045 1050 1055

His Gly Val Ala Asp Phe Tyr Glu Val Ile Leu Phe His Leu Ser Ala
 1060 1065 1070

Val Val Gln Phe Ala Leu Tyr Val Ser Cys Glu Asn Thr Ile Ser Asn
 1075 1080 1085

Lys Ala Ile Ser Ile Leu Lys Gly Val Ser Gln Ser Lys Phe Phe Val
 1090 1095 1100

Thr Arg Val Ser Ser Ser Ala Asp Pro Leu Leu Asn Asn Asp Arg Leu
 1105 1110 1115 1120

Ile Thr Thr Phe Glu Asn Ile Asp Glu Ser Ile Lys Ile Lys Phe Ala
 1125 1130 1135

Phe Ile Asp Lys Phe Glu Glu Leu Glu Asp Ser Leu Asn Met Lys Tyr
 1140 1145 1150

Glu Ile Leu Asp Phe Val Leu Gly Asn Leu Asn Gln Phe Asp Gly Lys
 1155 1160 1165

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Val Ala Thr Thr Ala His Phe Leu Leu Gly Tyr Lys Val Lys Gly Asp
 1170 1175 1180

Thr Leu Asp Leu Val Gln Thr Asn Asp Gln Asn Thr Leu Leu Lys Ser
 1185 1190 1195 1200

Phe Leu Asn Thr Leu Ser Ile Ser Leu Asp Leu Ile Ser Glu Ile Asp
 1205 1210 1215

Tyr Asn Asn Gly Asn Asn His Ile Ile Asp Val Gly Pro Ala Lys Leu
 1220 1225 1230

Ser Ser Leu Ile Leu Gln Ile Leu Ile Lys Leu Cys Gln Asp Pro Ile
 1235 1240 1245

Ser Ser Ser Ile Thr Leu Asn Gln Leu Arg Glu Tyr Glu Glu Leu Phe
 1250 1255 1260

Glu Lys Leu Val Asn Cys Gln Pro Lys Leu Asp Leu Asn Thr Val Trp
 1265 1270 1275 1280

Cys Gly Asn Gln Phe Asp Gly Asp Leu Gln Ile Asp Ala Ser Asn Val
 1285 1290 1295

Phe Val Asp Asn Gln Ala Ser Thr Gln Ala Phe Phe Ser Phe Ile Asn
 1300 1305 1310

Gln Arg Asn Leu Ile Leu Gln Tyr Leu Ser Leu Glu Phe His Ser Val
 1315 1320 1325

Lys Ser Arg Thr Lys Arg Glu Tyr Tyr Ser Lys Val Leu Thr Asn Asp
 1330 1335 1340

Lys Glu Phe Val Asn Arg Thr Pro Lys Val Leu Thr Phe Leu Asn Ile
 1345 1350 1355 1360

Leu Asn Tyr Ser Phe Lys Asn Phe Glu Val Gln Lys Tyr Glu Trp Leu
 1365 1370 1375

Asp Gln Lys Phe Asn Val Ser Leu Leu Leu Ala Glu Val Asn Ala Gln
 1380 1385 1390

Lys Asn Gly Thr Leu Asp Phe Ser Val Leu Thr Lys Val Phe Arg Leu
 1395 1400 1405

Leu Cys Gln Thr Ser Asn Leu Ile Thr Pro Glu Ser Lys Gln Leu Phe
 1410 1415 1420

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Ala Glu Glu Ile Met Val Glu Gly Ser Lys Ile Ser Asp Phe Val Thr
 425 1430 1435 1440

Lys Tyr Leu Val Ser Thr Asp Leu Lys Asp Val Gln Leu Lys Cys Leu
 1445 1450 1455

His Ser Trp Cys Gln Leu Ile Glu Ile Leu Val Thr Asp Ser Gly Ile
 1460 1465 1470

Asn Ser Leu Asn Phe Ile Leu Glu Val Leu Gln Val Ile Ile Pro Lys
 1475 1480 1485

Ile Asn Asp Tyr Phe Asp Val Asp Ile Leu Phe Ser Glu Glu Met Val
 1490 1495 1500

Ser Leu Cys Val Leu Leu Phe Asp Leu Tyr Asp Gln Leu Thr Leu Ala
 505 1510 1515 1520

Asp Arg Lys Gly Glu Asp Phe Ala Leu Gly Ile Glu Arg Leu Ile Pro
 1525 1530 1535

Leu Phe Gln Thr Cys Ile Ala Gly Ile Leu Asn Ser Asn Ser Thr Pro
 1540 1545 1550

Ser Leu Arg Ser Asp Leu Tyr Val Val Gly Asn Lys Phe Leu Leu Lys
 1555 1560 1565

Cys Phe Glu Arg Glu Ser Phe Leu Lys Gln Val Met His Ile Ile Lys
 1570 1575 1580

Ser Val Asp Lys Lys Phe Phe Gln Val Ile Cys Asn Asp Ala Ile Tyr
 585 1590 1595 1600

Ser Glu Gly Pro Ser Arg Ile Thr Ser Thr Leu Phe Leu Glu Ser Leu
 1605 1610 1615

Val His Leu Gly Thr Leu Val Lys Val Asp Phe Ile Leu Asn Ala Leu
 1620 1625 1630

Ile Lys Asn Asn Ala Leu Leu Leu Leu Val Arg Ser Val Lys Arg Thr
 1635 1640 1645

Asp Ala Met Ile Lys Leu Cys Gln Glu Lys Asn Ser Gly Val Thr Leu
 1650 1655 1660

Asp His Phe Ile Phe Asp Leu Met Ala Phe Lys Ala Thr Leu Tyr Phe
 665 1670 1675 1680

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Phe Val Arg Val Ala Lys Ser Lys Asn Gly Ala Leu Gln Leu Ile Gln
1685 1690 1695

Asn Glu Leu Phe Ser Ile Leu His Gln Ser Lys Phe Leu Gln Ile Asp
1700 1705 1710

Pro Asp Ile Gly Leu Ser Leu Arg Ile Glu Glu Val Gln Asp His Lys
1715 1720 1725

Thr Val Asn Val Asn Val Leu Leu Asp Thr Pro Leu Ser Ile Thr Asp
1730 1735 1740

Leu Val Asp Pro Tyr Lys Leu Arg Ser Glu Asn Thr Ile Ser Tyr Phe
745 1750 1755 1760

Glu Phe Leu Val Pro Ile Phe Gln Leu Leu Thr Thr Val Leu Leu Ser
1765 1770 1775

Met Gly Pro Asn Tyr Gln Pro Ala Ile Ile Gln Thr Arg Glu Leu Met
1780 1785 1790

Lys Ser Val Asn Arg Leu Val Val Gly Val Met Lys Arg Asp Phe Leu
1795 1800 1805

Val Glu Thr Lys Gln Ile Gly Gln Gly Leu Tyr Lys Glu Glu Ser His
1810 1815 1820

Glu Leu Val Ser Leu Lys Glu Leu Val Lys Leu Phe Ile Leu Ile Asp
825 1830 1835 1840

Ser Leu Ala His Tyr Ser Val
1845

SEQUENCE LISTING

45/83

<110> Hoechst Marion Roussel

<120> ESSENTIAL GENES FROM C. ALBICANS AND A METHOD FOR
SCREENING ANTIMYCOTIC SUBSTANCES USING SAID GENES

<130> SEQID08

<140>

<141>

<160> 1

<170> PatentIn Ver. 2.1

<210> 1

<211> 575

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:homologous
fragment to Sc YJL039c

<400> 1

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taattgcagg ttgataattt ggtcccattg acaataacac tgttgtaagt agctgaaata 120
ttggtacaag gaactcaaaa tatgatatag tgttttcact tcgcaacttg tatggatcca 180
ccaagtcagt tatcgaaagt ggagtatcta gcaaaacatt tacattgaca gtcttgatgat 240
cttgaacttc ttcaattcgt aaacttaaac caatatctgg atcaatctgc aaaaacttcg 300
actgatgcaa aattgaaaac aattcatttt ggaatcannn nnanaantna aaaaaaatat 360
atattntntt tttttttttt ttntttnttt tttattttat cttacannac accccaacac 420
aacaccaaac cnaaaaacac ccaacacctc catcttgccc cgcttttctc tcacattttt 480
tctctactac tatcacacaa tctataaaac atacaccccc tcaaccctc ctccccaaca 540
aacctacctc cctcaactcc tatttcctcc cttcc
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575

46/83
SEQUENCE LISTING

<110> Hoechst Marion Roussel

<120> ESSENTIAL GENES FROM C. ALBICANS AND A METHOD FOR
SCREENING ANTIMYCOTIC SUBSTANCES USING SAID GENES

<130> SEQID09

<140>

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<160> 2

<170> PatentIn Ver. 2.1

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<211> 921

<212> DNA

<213> Candida albicans

<220>

<221> CDS

<222> (1)..(918)

<220>

<221> gene

<222> (1)..(918)

<223> Gene CaOR110

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1				5					10					15		

tgg	tta	cca	cca	cca	cac	cca	cca	aat	cct	act	ggg	att	gac	agt	gac	96
Trp	Leu	Pro	Pro	Pro	His	Pro	Pro	Asn	Pro	Thr	Gly	Ile	Asp	Ser	Asp	
			20					25					30			

ccg	gct	tta	gca	cca	cat	ggg	gtt	gaa	caa	gcc	caa	cag	tta	gct	gcc	144
Pro	Ala	Leu	Ala	Pro	His	Gly	Val	Glu	Gln	Ala	Gln	Gln	Leu	Ala	Ala	
			35				40					45				

tat	ctt	aca	tca	tta	cct	aca	cat	gaa	aag	cct	gaa	ttt	att	att	gct	192
Tyr	Leu	Thr	Ser	Leu	Pro	Thr	His	Glu	Lys	Pro	Glu	Phe	Ile	Ile	Ala	
			50				55					60				

tca	cct	ttt	tat	cgt	tgt	ata	gaa	acg	tcg	aga	ccc	att	gcc	gaa	atg	240
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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Ser	Pro	Phe	Tyr	Arg	Cys	Ile	Glu	Thr	Ser	Arg	Pro	Ile	Ala	Glu	Met	
65					70				75						80	
ttg	gac	ttg	aag	att	gct	tta	gaa	aga	gga	gtt	ggt	gaa	tgg	ttt	cgt	288
Leu	Asp	Leu	Lys	Ile	Ala	Leu	Glu	Arg	Gly	Val	Gly	Glu	Trp	Phe	Arg	
				85					90					95		
aaa	aat	aga	gat	acc	aaa	cca	gtt	ccc	ggt	gat	tac	aca	caa	ttg	aga	336
Lys	Asn	Arg	Asp	Thr	Lys	Pro	Val	Pro	Gly	Asp	Tyr	Thr	Gln	Leu	Arg	
				100					105					110		
aca	ttt	ttc	gat	aaa	tta	ttg	atc	gat	gaa	gat	act	tgg	cca	aga	gat	384
Thr	Phe	Phe	Asp	Lys	Leu	Leu	Ile	Asp	Glu	Asp	Thr	Trp	Pro	Arg	Asp	
				115					120					125		
aac	tta	aat	gtt	ata	cct	aat	att	gaa	gga	gaa	gat	tat	gat	gaa	atc	432
Asn	Leu	Asn	Val	Ile	Pro	Asn	Ile	Glu	Gly	Glu	Asp	Tyr	Asp	Glu	Ile	
				130					135					140		
tac	gat	cgt	gcc	aaa	ttg	ttt	tgg	aaa	aag	ttt	att	cct	gaa	ttt	gaa	480
Tyr	Asp	Arg	Ala	Lys	Leu	Phe	Trp	Lys	Lys	Phe	Ile	Pro	Glu	Phe	Glu	
				145					150					155		160
aag	aaa	ttc	ccc	gaa	att	aaa	aat	gtg	ttg	ata	gtt	aca	cat	gca	gca	528
Lys	Lys	Phe	Pro	Glu	Ile	Lys	Asn	Val	Leu	Ile	Val	Thr	His	Ala	Ala	
				165					170					175		
acg	aaa	att	gct	tta	gga	tca	gct	tta	tta	cag	tta	aaa	tca	gtt	act	576
Thr	Lys	Ile	Ala	Leu	Gly	Ser	Ala	Leu	Leu	Gln	Leu	Lys	Ser	Val	Thr	
				180					185					190		
gat	gtt	ata	gat	gat	aat	caa	act	gtg	tta	cgt	gct	ggt	gca	tgt	tca	624
Asp	Val	Ile	Asp	Asp	Asn	Gln	Thr	Val	Leu	Arg	Ala	Gly	Ala	Cys	Ser	
				195					200					205		
tta	tcc	aaa	ttt	gtt	aga	gat	ggc	gaa	gat	aaa	acc	aat	cat	act	att	672
Leu	Ser	Lys	Phe	Val	Arg	Asp	Gly	Glu	Asp	Lys	Thr	Asn	His	Thr	Ile	
				210					215					220		
caa	tgg	aaa	att	gtc	atg	aat	ggt	aat	tgt	gaa	ttc	ttg	aca	cag	ggt	720
Gln	Trp	Lys	Ile	Val	Met	Asn	Gly	Asn	Cys	Glu	Phe	Leu	Thr	Gln	Gly	
				225					230					235		240
gaa	gaa	atg	aac	tgg	gat	ttc	cgt	cgt	ggt	gtt	gaa	gac	ggg	tca	gct	768
Glu	Glu	Met	Asn	Trp	Asp	Phe	Arg	Arg	Gly	Val	Glu	Ala	Gly	Ser	Ala	
				245					250					255		
gaa	gat	ata	gcg	caa	aga	aag	gca	gca	gca	gaa	gca	gaa	gca	aaa	gca	816

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Glu Asp Ile Ala Gln Arg Lys Ala Ala Ala Glu Ala Glu Ala Lys Ala
 260 265 270

ttg aag aaa aat gaa caa acc aaa tcc gat ggt ccc atc act gaa tct 864
 Leu Lys Lys Asn Glu Gln Thr Lys Ser Asp Gly Pro Ile Thr Glu Ser
 275 280 285

gcc act ggg gca gaa ata gat ggg aat gaa gat gaa ttt gaa gta cgt 912
 Ala Thr Gly Ala Glu Ile Asp Gly Asn Glu Asp Glu Phe Glu Val Arg
 290 295 300

aaa act tga 921
 Lys Thr
 305

<210> 2

<211> 306

<212> PRT

<213> Candida albicans

<400> 2

Met Thr Ile Glu Thr Ile Tyr Ile Ala Arg His Gly Tyr Arg Ser Asn
 1 5 10 15

Trp Leu Pro Pro Pro His Pro Pro Asn Pro Thr Gly Ile Asp Ser Asp
 20 25 30

Pro Ala Leu Ala Pro His Gly Val Glu Gln Ala Gln Gln Leu Ala Ala
 35 40 45

Tyr Leu Thr Ser Leu Pro Thr His Glu Lys Pro Glu Phe Ile Ile Ala
 50 55 60

Ser Pro Phe Tyr Arg Cys Ile Glu Thr Ser Arg Pro Ile Ala Glu Met
 65 70 75 80

Leu Asp Leu Lys Ile Ala Leu Glu Arg Gly Val Gly Glu Trp Phe Arg
 85 90 95

Lys Asn Arg Asp Thr Lys Pro Val Pro Gly Asp Tyr Thr Gln Leu Arg
 100 105 110

Thr Phe Phe Asp Lys Leu Leu Ile Asp Glu Asp Thr Trp Pro Arg Asp
 115 120 125

Asn Leu Asn Val Ile Pro Asn Ile Glu Gly Glu Asp Tyr Asp Glu Ile
 130 135 140

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Tyr Asp Arg Ala Lys Leu Phe Trp Lys Lys Phe Ile Pro Glu Phe Glu
 145 150 155 160

Lys Lys Phe Pro Glu Ile Lys Asn Val Leu Ile Val Thr His Ala Ala
 165 170 175

Thr Lys Ile Ala Leu Gly Ser Ala Leu Leu Gln Leu Lys Ser Val Thr
 180 185 190

Asp Val Ile Asp Asp Asn Gln Thr Val Leu Arg Ala Gly Ala Cys Ser
 195 200 205

Leu Ser Lys Phe Val Arg Asp Gly Glu Asp Lys Thr Asn His Thr Ile
 210 215 220

Gln Trp Lys Ile Val Met Asn Gly Asn Cys Glu Phe Leu Thr Gln Gly
 225 230 235 240

Glu Glu Met Asn Trp Asp Phe Arg Arg Gly Val Glu Ala Gly Ser Ala
 245 250 255

Glu Asp Ile Ala Gln Arg Lys Ala Ala Ala Glu Ala Glu Ala Lys Ala
 260 265 270

Leu Lys Lys Asn Glu Gln Thr Lys Ser Asp Gly Pro Ile Thr Glu Ser
 275 280 285

Ala Thr Gly Ala Glu Ile Asp Gly Asn Glu Asp Glu Phe Glu Val Arg
 290 295 300

Lys Thr
 305

50/83
SEQUENCE LISTING

<110> Hoechst Marion Roussel

<120> ESSENTIAL GENES FROM C. ALBICANS AND A METHOD FOR
SCREENING ANTIMYCOTIC SUBSTANCES USING SAID GENES

<130> SEQID10

<140>

<141>

<160> 2

<170> PatentIn Ver. 2.1

<210> 1

<211> 1454

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(1452)

<223> Gene CaOR110 Splice Variant

<220>

<223> Description of Artificial Sequence:Splice Vaiant

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1 5 10 15	
tgg tta cca cca cca cac cca cca aat cct act ggt att gac agt gac	96
Trp Leu Pro Pro Pro His Pro Pro Asn Pro Thr Gly Ile Asp Ser Asp	
20 25 30	
ccg gct tta gca cca cat ggt gtt gaa caa gcc caa cag tta gct gcc	144
Pro Ala Leu Ala Pro His Gly Val Glu Gln Ala Gln Gln Leu Ala Ala	
35 40 45	
tat ctt aca tca tta cct aca cat gaa aag cct gaa ttt att att gct	192
Tyr Leu Thr Ser Leu Pro Thr His Glu Lys Pro Glu Phe Ile Ile Ala	
50 55 60	
tca cct ttt tat cgt tgt ata gaa acg tcg aga ccc att gcc gaa atg	240
Ser Pro Phe Tyr Arg Cys Ile Glu Thr Ser Arg Pro Ile Ala Glu Met	

5183

65	70	75	80	
ttg gac ttg aag att gct tta gaa aga gga gtt ggt gaa tgg ttt cgt				288
Leu Asp Leu Lys Ile Ala Leu Glu Arg Gly Val Gly Glu Trp Phe Arg				
	85	90	95	
aaa aat aga gat acc aaa cca gtt ccc ggt gat tac aca caa ttg aga				336
Lys Asn Arg Asp Thr Lys Pro Val Pro Gly Asp Tyr Thr Gln Leu Arg				
	100	105	110	
aca ttt ttc gat aaa tta ttg atc gat gaa gat act tgg cca aga gat				384
Thr Phe Phe Asp Lys Leu Leu Ile Asp Glu Asp Thr Trp Pro Arg Asp				
	115	120	125	
aac tta aat gtt ata cct aat att gaa gga gaa gat tat gat gaa atc				432
Asn Leu Asn Val Ile Pro Asn Ile Glu Gly Glu Asp Tyr Asp Glu Ile				
	130	135	140	
tac gat cgt gcc aaa ttg ttt tgg aaa aag ttt att cct gaa ttt gaa				480
Tyr Asp Arg Ala Lys Leu Phe Trp Lys Lys Phe Ile Pro Glu Phe Glu				
	145	150	155	160
aag aaa ttc ccc gaa att aaa aat gtg ttg ata gtt aca cat gca gca				528
Lys Lys Phe Pro Glu Ile Lys Asn Val Leu Ile Val Thr His Ala Ala				
	165	170	175	
acg aaa att gct tta gga tca gct tta tta cag tta aaa tca gtt act				576
Thr Lys Ile Ala Leu Gly Ser Ala Leu Leu Gln Leu Lys Ser Val Thr				
	180	185	190	
gat gtt ata gat gat aat caa act gtg tta cgt gct ggt gca tgt tca				624
Asp Val Ile Asp Asp Asn Gln Thr Val Leu Arg Ala Gly Ala Cys Ser				
	195	200	205	
tta tcc aaa ttt gtt aga gat ggc gaa gat aaa acc aat cat act att				672
Leu Ser Lys Phe Val Arg Asp Gly Glu Asp Lys Thr Asn His Thr Ile				
	210	215	220	
caa tgg aaa att gtc atg aat ggt aat tgt gaa ttc ttg aca cag ggt				720
Gln Trp Lys Ile Val Met Asn Gly Asn Cys Glu Phe Leu Thr Gln Gly				
	225	230	235	240
gaa gaa atg aac tgg gat ttc cgt cgt ggt gtt gaa gcc ggg tca gct				768
Glu Glu Met Asn Trp Asp Phe Arg Arg Gly Val Glu Ala Gly Ser Ala				
	245	250	255	
gaa gat ata gcg caa aga aag gca gca gca gaa gca gaa gca aaa gca				816
Glu Asp Ile Ala Gln Arg Lys Ala Ala Ala Glu Ala Glu Ala Lys Ala				

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260	265	270	
ttg aag aaa aat gaa caa acc aaa tcc gat ggt ccc atc act gaa tct			864
Leu Lys Lys Asn Glu Gln Thr Lys Ser Asp Gly Pro Ile Thr Glu Ser			
275	280	285	
gcc act ggg gca gaa ata gat ggg aat gaa gat gaa ttt gaa aca ttt			912
Ala Thr Gly Ala Glu Ile Asp Gly Asn Glu Asp Glu Phe Glu Thr Phe			
290	295	300	
tat gta acc atc gat ata cct tca att tcg aat aaa atc gac aat gaa			960
Tyr Val Thr Ile Asp Ile Pro Ser Ile Ser Asn Lys Ile Asp Asn Glu			
305	310	315	320
gaa gaa cca cca tca agg aca ggt caa gct cca aaa ttc aaa aac aat			1008
Glu Glu Pro Pro Ser Arg Thr Gly Gln Ala Pro Lys Phe Lys Asn Asn			
325	330	335	
att atc aag cct tca gca caa ctc caa ttt act gat tta aaa gaa gat			1056
Ile Ile Lys Pro Ser Ala Gln Leu Gln Phe Thr Asp Leu Lys Glu Asp			
340	345	350	
cat cca tta gta aaa ata tcg aac aat act ata tct gct caa ggc tcg			1104
His Pro Leu Val Lys Ile Ser Asn Asn Thr Ile Ser Ala Gln Gly Ser			
355	360	365	
tcg tcg tcg tcg tta tca gcg tcg aaa aat gga ttt aat agt cat act			1152
Ser Ser Ser Ser Leu Ser Ala Ser Lys Asn Gly Phe Asn Ser His Thr			
370	375	380	
cac aat tca gga gtc att gat cca tca gca ctt ata gat ggg aaa att			1200
His Asn Ser Gly Val Ile Asp Pro Ser Ala Leu Ile Asp Gly Lys Ile			
385	390	395	400
tat cag act gat tgg aat caa tta caa ggt act gaa cta ata ttt gat			1248
Tyr Gln Thr Asp Trp Asn Gln Leu Gln Gly Thr Glu Leu Ile Phe Asp			
405	410	415	
gaa aat ggt caa ttt ata ggc aag gtt aag gaa cat ttg act tgc aat			1296
Glu Asn Gly Gln Phe Ile Gly Lys Val Lys Glu His Leu Thr Cys Asn			
420	425	430	
aat aac aca aaa ttc aca tta aaa aag gca gaa gaa gta gaa caa ctt			1344
Asn Asn Thr Lys Phe Thr Leu Lys Lys Ala Glu Glu Val Glu Gln Leu			
435	440	445	
cgt tca gca gat gat tct atc atg gat ata gat caa gac tca caa gga			1392
Arg Ser Ala Asp Asp Ser Ile Met Asp Ile Asp Gln Asp Ser Gln Gly			

53183

450

455

460

caa caa cca gct aga agt cag ttc tta aaa aga gca att gtg gct gct 1440
 Gln Gln Pro Ala Arg Ser Gln Phe Leu Lys Arg Ala Ile Val Ala Ala
 465 470 475 480

aga gcc aaa ggt aa 1454
 Arg Ala Lys Gly

<210> 2

<211> 484

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence:Splice Vaiaant

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Met Thr Ile Glu Thr Ile Tyr Ile Ala Arg His Gly Tyr Arg Ser Asn
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Trp Leu Pro Pro Pro His Pro Pro Asn Pro Thr Gly Ile Asp Ser Asp
 20 25 30

Pro Ala Leu Ala Pro His Gly Val Glu Gln Ala Gln Gln Leu Ala Ala
 35 40 45

Tyr Leu Thr Ser Leu Pro Thr His Glu Lys Pro Glu Phe Ile Ile Ala
 50 55 60

Ser Pro Phe Tyr Arg Cys Ile Glu Thr Ser Arg Pro Ile Ala Glu Met
 65 70 75 80

Leu Asp Leu Lys Ile Ala Leu Glu Arg Gly Val Gly Glu Trp Phe Arg
 85 90 95

Lys Asn Arg Asp Thr Lys Pro Val Pro Gly Asp Tyr Thr Gln Leu Arg
 100 105 110

Thr Phe Phe Asp Lys Leu Leu Ile Asp Glu Asp Thr Trp Pro Arg Asp
 115 120 125

Asn Leu Asn Val Ile Pro Asn Ile Glu Gly Glu Asp Tyr Asp Glu Ile
 130 135 140

Tyr Asp Arg Ala Lys Leu Phe Trp Lys Lys Phe Ile Pro Glu Phe Glu
 145 150 155 160

Lys Lys Phe Pro Glu Ile Lys Asn Val Leu Ile Val Thr His Ala Ala

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165	170	175
Thr Lys Ile Ala Leu Gly Ser Ala Leu Leu Gln Leu Lys Ser Val Thr		
180	185	190
Asp Val Ile Asp Asp Asn Gln Thr Val Leu Arg Ala Gly Ala Cys Ser		
195	200	205
Leu Ser Lys Phe Val Arg Asp Gly Glu Asp Lys Thr Asn His Thr Ile		
210	215	220
Gln Trp Lys Ile Val Met Asn Gly Asn Cys Glu Phe Leu Thr Gln Gly		
225	230	235
Glu Glu Met Asn Trp Asp Phe Arg Arg Gly Val Glu Ala Gly Ser Ala		
245	250	255
Glu Asp Ile Ala Gln Arg Lys Ala Ala Ala Glu Ala Glu Ala Lys Ala		
260	265	270
Leu Lys Lys Asn Glu Gln Thr Lys Ser Asp Gly Pro Ile Thr Glu Ser		
275	280	285
Ala Thr Gly Ala Glu Ile Asp Gly Asn Glu Asp Glu Phe Glu Thr Phe		
290	295	300
Tyr Val Thr Ile Asp Ile Pro Ser Ile Ser Asn Lys Ile Asp Asn Glu		
305	310	315
Glu Glu Pro Pro Ser Arg Thr Gly Gln Ala Pro Lys Phe Lys Asn Asn		
325	330	335
Ile Ile Lys Pro Ser Ala Gln Leu Gln Phe Thr Asp Leu Lys Glu Asp		
340	345	350
His Pro Leu Val Lys Ile Ser Asn Asn Thr Ile Ser Ala Gln Gly Ser		
355	360	365
Ser Ser Ser Ser Leu Ser Ala Ser Lys Asn Gly Phe Asn Ser His Thr		
370	375	380
His Asn Ser Gly Val Ile Asp Pro Ser Ala Leu Ile Asp Gly Lys Ile		
385	390	395
Tyr Gln Thr Asp Trp Asn Gln Leu Gln Gly Thr Glu Leu Ile Phe Asp		
405	410	415
Glu Asn Gly Gln Phe Ile Gly Lys Val Lys Glu His Leu Thr Cys Asn		

55183

420

425

430

Asn Asn Thr Lys Phe Thr Leu Lys Lys Ala Glu Glu Val Glu Gln Leu
435 440 445

Arg Ser Ala Asp Asp Ser Ile Met Asp Ile Asp Gln Asp Ser Gln Gly
450 455 460

Gln Gln Pro Ala Arg Ser Gln Phe Leu Lys Arg Ala Ile Val Ala Ala
465 470 475 480

Arg Ala Lys Gly

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SEQUENCE LISTING

<110> Hoechst Marion Roussel

<120> ESSENTIAL GENES FROM C. ALBICANS AND A METHOD FOR
SCREENING ANTIMYCOTIC SUBSTANCES USING SAID GENES

<130> SEQID11

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<160> 2

<170> PatentIn Ver. 2.1

<210> 1

<211> 2877

<212> DNA

<213> Candida albicans

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<221> CDS

<222> (1)..(2874)

<220>

<221> gene

<222> (1)..(2874)

<223> Gene CaMR212

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1 5 10 15	

cct gct ggg aaa gca gtg gac aaa aaa ccc aac tcg tcc gag tta agt	96
Pro Ala Gly Lys Ala Val Asp Lys Lys Pro Asn Ser Ser Glu Leu Ser	
20 25 30	

tat tta tta tac tat gca tcc act cgt aga gtc aaa tta gaa aag gtg	144
Tyr Leu Leu Tyr Tyr Ala Ser Thr Arg Arg Val Lys Leu Glu Lys Val	
35 40 45	

att aat ttt ttg aaa gat aaa act cat cat gat gtt ggt aga aac cgt	192
Ile Asn Phe Leu Lys Asp Lys Thr His His Asp Val Gly Arg Asn Arg	
50 55 60	

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acc gat ttg gag tgg gga gtc tca ttc ttg gaa tta tgt att act tgg	912
Thr Asp Leu Glu Trp Gly Val Ser Phe Leu Glu Leu Cys Ile Thr Trp	
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Ile Pro Val Gln Leu Arg Phe Val Ser Leu Ser Thr Leu Leu Ala Thr	
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Leu Gly Arg Ile Asn Ile Glu Gly Asn Thr Lys Ser Asn Tyr Asn Met	
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caa ttc cag tat gct cgt tac ttg tta gga tta ctt tca tct cgt gtg	1056
Gln Phe Gln Tyr Ala Arg Tyr Leu Leu Gly Leu Leu Ser Ser Arg Val	
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Asn Met Ile Gly Leu Ser Val Ser Asp Ile Ile Gln Gln Leu Leu Ser	
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Leu Gln Ala Asp Leu Ile Leu Lys Ala Ser Asp Leu Asp Lys Ser Glu	
370 375 380	
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Ile Ser Ile Leu Thr Asp Ile Tyr Ser Asp Cys Ile Cys Ser Leu Thr	
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Thr His Ile Tyr Tyr Phe Asp Gln Val Pro Asp Ser Ile Gln Glu Ile	
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tta atc aag att gat tac att tta gaa agc agt ttt gtg gaa gat aat	1296
Leu Ile Lys Ile Asp Tyr Ile Leu Glu Ser Ser Phe Val Glu Asp Asn	
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aac att acg tcc act gga gaa caa att caa gat ttg att atc caa ttg	1344
Asn Ile Thr Ser Thr Gly Glu Gln Ile Gln Asp Leu Ile Ile Gln Leu	
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Leu Asp Asn Ile Ser Lys Ile Phe Leu Ile Leu Lys Asn Lys Ser Ser
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tca att aat cgt aac cat gtg aat ttg gaa cat tgg gat atc agt tta 1440
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gga tta ttg gct cca caa ggc gac cat gat gat aac aga aaa atg att 1488
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Lys Ser Ser Lys Leu Phe Lys Gln Ile Leu Asp Ala Val Glu Tyr Arg	
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Cys Gly Asn Asn Phe Leu Ile Val Trp Leu His Pro Gln Lys Gln Leu	
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770	775 780
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Ser Leu Ala Leu Ser Gly Gly Ala Asp His Gly Gly His Phe Val Pro	
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cca cct gaa ttt gtt aac cac acc ggt ttg tct tct gaa tct gcg tca	2448
Pro Pro Glu Phe Val Asn His Thr Gly Leu Ser Ser Glu Ser Ala Ser	
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tca aac tca gag aaa ggt ttg tat act ggt tta gga ttg ggt act gct	2496
Ser Asn Ser Glu Lys Gly Leu Tyr Thr Gly Leu Gly Leu Gly Thr Ala	
820	825 830
ggt gat att act atg att cat tct gaa ata tta caa tac agt caa cat	2544

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 865 870 875 880

tat gat agt aaa tat ttg cag tca cca aga gta agt gat ttg aaa gat 2688
 Tyr Asp Ser Lys Tyr Leu Gln Ser Pro Arg Val Ser Asp Leu Lys Asp
 885 890 895

gcc atg tca aca cat agg ggt ata agg tta tct aaa cca aat ttt ggt 2736
 Ala Met Ser Thr His Arg Gly Ile Arg Leu Ser Lys Pro Asn Phe Gly
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ggt gcc aat gga act gct aat atg acg gat tct gct tct aca tcc aat 2784
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<213> Candida albicans

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 Lys Cys Ser Glu Asn Leu Asn Val Phe Ala Phe Gln Val Cys Tyr Ile
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 Leu Gln Leu Ile Ala Asn Thr Lys Asp Leu Ala Leu Cys Lys Asn Val
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 Val Lys Thr Phe Gly Val Leu Cys Glu Asn Leu Asp Gly Gly Leu Phe
 115 120 125
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 130 135 140
 Leu Val Ser Phe Gly Lys Asp Arg Ser Gly Val Thr Gln Tyr Asp Trp
 145 150 155 160
 Gln Met Ile Ser Leu Met Ala Ile Asn Asp Ile Ser Ser Cys Leu Ser
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 Tyr Asn Ala Ala Val Gly Lys Lys Phe Ile Ala Leu Ser Ile Pro Val
 180 185 190
 Leu Leu Gln Phe Ile Ile Ala Asn Asn Pro Gln Ser Ser Ile Leu Gln
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 Arg Leu Lys Ser Asn Leu His Val Glu Asp Asp Gly Lys Arg Leu Ser
 210 215 220
 Arg Ala His Leu Gln Lys Ser His Ser Lys Ile Ala Gln Gln Ile Asp
 225 230 235 240
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 245 250 255
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 275 280 285
 Thr Asp Leu Glu Trp Gly Val Ser Phe Leu Glu Leu Cys Ile Thr Trp
 290 295 300
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 340 345 350
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 Leu Gln Ala Asp Leu Ile Leu Lys Ala Ser Asp Leu Asp Lys Ser Glu
 370 375 380
 Ile Ser Ile Leu Thr Asp Ile Tyr Ser Asp Cys Ile Cys Ser Leu Thr
 385 390 395 400
 Thr His Ile Tyr Tyr Phe Asp Gln Val Pro Asp Ser Ile Gln Glu Ile
 405 410 415
 Leu Ile Lys Ile Asp Tyr Ile Leu Glu Ser Ser Phe Val Glu Asp Asn
 420 425 430
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 435 440 445
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 Ser Ile Asn Arg Asn His Val Asn Leu Glu His Trp Asp Ile Ser Leu
 465 470 475 480
 Gly Leu Leu Ala Pro Gln Gly Asp His Asp Asp Asn Arg Lys Met Ile
 485 490 495
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 500 505 510
 Phe Asp Glu Phe Leu Asn Asn Glu Leu Ala Val Gly Asn Ser Lys Lys
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 530 535 540
 Ala Val Glu Gly Val Asn Lys Ser Asp Asp Leu Asp Asn Gly Lys Asp
 545 550 555 560
 Phe Lys Lys Pro Asp Ala Asn Gln Tyr Ile Thr Asn Gln Gln Asn Phe

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Met Met Asn Ile Leu Gly Leu Asn Phe Leu Ser Asn Phe Ile Pro Phe		
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625	630	635 640
Arg Gln Lys Phe Lys Asp Thr Phe Ala His Ile Ile Leu Tyr Tyr Met		
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Leu Lys Asp Leu Asp Glu Gln Tyr Ser His Asp Leu Gln Asn Tyr Cys		
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Lys Ser Ser Lys Leu Phe Lys Gln Ile Leu Asp Ala Val Glu Tyr Arg		
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Lys Met Gln Lys Phe Trp Val His Gly Ile Asp Pro Ser Pro Ser Asp		
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Asn Tyr Ile Ala Ile Arg Ile Lys Pro Glu Asn Ile Glu Glu Phe Ala		
725	730	735
Cys Gly Asn Asn Phe Leu Ile Val Trp Leu His Pro Gln Lys Gln Leu		
740	745	750
Leu Thr Glu Ile Glu Lys Ser Gln Val Ser Thr His Met Ser Thr Phe		
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Asn Asn Asp Ser Arg Asn Thr Asn Met Thr Val Ile Met Asp Gln Gly		
770	775	780
Ser Leu Ala Leu Ser Gly Gly Ala Asp His Gly Gly His Phe Val Pro		
785	790	795 800
Pro Pro Glu Phe Val Asn His Thr Gly Leu Ser Ser Glu Ser Ala Ser		
805	810	815
Ser Asn Ser Glu Lys Gly Leu Tyr Thr Gly Leu Gly Leu Gly Thr Ala		

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Tyr Asp Ser Lys Tyr Leu Gln Ser Pro Arg Val Ser Asp Leu Lys Asp		
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Ala Met Ser Thr His Arg Gly Ile Arg Leu Ser Lys Pro Asn Phe Gly		
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SEQUENCE LISTING

<110> Hoechst Marion Roussel

<120> ESSENTIAL GENES FROM C. ALBICANS AND A METHOD FOR
SCREENING ANTIMYCOTIC SUBSTANCES USING SAID GENES

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fragment to Sc YMR212c

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67183

SEQUENCE LISTING

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 100 105 110
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 225 230 235 240
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63183

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70183

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 515 520 525

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atg aca tta act gaa gat aaa tta cct gat gcg tta ata tca gtg gca 1968

71183

Met Thr Leu Thr Glu Asp Lys Leu Pro Asp Ala Leu Ile Ser Val Ala
645 650 655

ctt aga gta tta cga gca ctt tct ata aat gaa aaa gat ttt gtt tcc 2016
Leu Arg Val Leu Arg Ala Leu Ser Ile Asn Glu Lys Asp Phe Val Ser
660 665 670

atg gcg gta gaa ata att act gat att cgt gat tct cga gat gat gaa 2064
Met Ala Val Glu Ile Ile Thr Asp Ile Arg Asp Ser Arg Asp Asp Glu
675 680 685

gag ttc cat tct gct gcc gct aca ttt gat gat gat gat gat gat att 2112
Glu Phe His Ser Ala Ala Ala Thr Phe Asp Asp Asp Asp Asp Asp Ile
690 695 700

ttg gga aat ggt gat gat gaa tct caa caa tca tca tca ctc agt gca 2160
Leu Gly Asn Gly Asp Asp Glu Ser Gln Gln Ser Ser Ser Leu Ser Ala
705 710 715 720

gta aca aag aag cga aga att gaa cca gat atg cca cca gat gat att 2208
Val Thr Lys Lys Arg Arg Ile Glu Pro Asp Met Pro Pro Asp Asp Ile
725 730 735

gtg tta aga tgt ctt acc atg aca caa tat gta ttg gaa gta att act 2256
Val Leu Arg Cys Leu Thr Met Thr Gln Tyr Val Leu Glu Val Ile Thr
740 745 750

cat agt ttg gat gat cat ctt tca ttg agt tct att tac agt ggt att 2304
His Ser Leu Asp Asp His Leu Ser Leu Ser Ser Ile Tyr Ser Gly Ile
755 760 765

gtc aat tat gct att cag aat gaa tcg aaa aag aaa tta tat ctt gct 2352
Val Asn Tyr Ala Ile Gln Asn Glu Ser Lys Lys Lys Leu Tyr Leu Ala
770 775 780

ggg tta act tgt tta gga ctt tat tct tta att gat tcc aaa att gcc 2400
Gly Leu Thr Cys Leu Gly Leu Tyr Ser Leu Ile Asp Ser Lys Ile Ala
785 790 795 800

aga att gca act aca aca tta tta ctg gca atg aga agt aat ggt gaa 2448
Arg Ile Ala Thr Thr Thr Leu Leu Leu Ala Met Arg Ser Asn Gly Glu
805 810 815

gaa gtg aaa gag att gga atg aaa gct att gtg gat ata ttg gca att 2496
Glu Val Lys Glu Ile Gly Met Lys Ala Ile Val Asp Ile Leu Ala Ile
820 825 830

tat ggt atg agt att ctt gat aaa tca tct aaa tac aaa tat tca aga 2544

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Tyr Gly Met Ser Ile Leu Asp Lys Ser Ser Lys Tyr Lys Tyr Ser Arg
 835 840 845

atg ttt ttc aaa gtt tta aat tca ttt gat gca cca aaa tta caa tgc 2592
 Met Phe Phe Lys Val Leu Asn Ser Phe Asp Ala Pro Lys Leu Gln Cys
 850 855 860

att gtc gct gaa gga tta tgc aaa ttg ttt tta gcc gat att ttg tac 2640
 Ile Val Ala Glu Gly Leu Cys Lys Leu Phe Leu Ala Asp Ile Leu Tyr
 865 870 875 880

aag act gac aaa cgg agt tta ttt gga aat gct att caa ggt ggt ggt 2688
 Lys Thr Asp Lys Arg Ser Leu Phe Gly Asn Ala Ile Gln Gly Gly Gly
 885 890 895

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 Gly Gly Gly Gly Gly Asn Asp Asp Pro Thr Thr Thr Asn Asp Asp Glu
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act gaa gaa gaa aca gat cga gag cat gaa aag cat tta ttt gaa gcg 2784
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 915 920 925

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 Ile Val Leu Ile Tyr Phe Asn Pro Asn Thr Lys Ser Asn Gln Glu Leu
 930 935 940

caa caa att ttg tca ttt tgt att cca gtt tat gcc ttt tct cat ata 2880
 Gln Gln Ile Leu Ser Phe Cys Ile Pro Val Tyr Ala Phe Ser His Ile
 945 950 955 960

aat cat caa atc aat tta gct gca gtt agt ggt gat gtt att tat cga 2928
 Asn His Gln Ile Asn Leu Ala Ala Val Ser Gly Asp Val Ile Tyr Arg
 965 970 975

ctt ttc act gaa aca gaa aca gaa tta tca cca agt gtt ata atc cct 2976
 Leu Phe Thr Glu Thr Glu Thr Glu Leu Ser Pro Ser Val Ile Ile Pro
 980 985 990

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 Gln Leu Ile Ser Trp Cys Asp Pro Arg Asn Leu Val Lys Leu Ser Asn
 995 1000 1005

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tta caa gtg gtt gaa caa gta gat gct cgt aat gtt aaa aga tgc atc 3120

73/83

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 Ile Asn Asn Leu Asn Lys Phe His Ile Thr Glu Glu Leu Glu Ser Asn
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 Gln Leu Gln Ala Leu Ile Lys Ala Leu Asp Ala Thr Val Glu Leu Phe
 1060 1065 1070
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 1075 1080 1085
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 Lys Asn Phe Asp Thr Phe Ile Glu Ser Ile Lys Asn Lys Leu Glu Ile
 1090 1095 1100
 gct caa aaa aga gaa gaa aat gaa ctg att aaa agt ggt aca aat tca 3360
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 1125 1130 1135
 caa ata tct ata aaa tca gaa aca aaa aga aga gat ctg gat cga tct 3456
 Gln Ile Ser Ile Lys Ser Glu Thr Lys Arg Arg Asp Leu Asp Arg Ser
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 1155 1160 1165
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 Glu Glu Asp Asp Asn Glu Glu Glu Glu Gln Glu Lys Lys Lys Ser Phe
 1170 1175 1180
 act gat gga aaa aat aaa ctt gaa cta aag gca gat aag cca atc aca 3600
 Thr Asp Gly Lys Asn Lys Leu Glu Leu Lys Ala Asp Lys Pro Ile Thr
 1185 1190 1195 1200
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 Phe Lys Ala Glu Asp Lys Arg Glu Gly Ser Val Glu Thr Asp His Gly
 1205 1210 1215
 caa gaa caa gtt cta gtt gaa tca aag aaa gtc att gat agt aat gtt 3696

74183

Gln Glu Gln Val Leu Val Glu Ser Lys Lys Val Ile Asp Ser Asn Val
 1220 1225 1230

gaa gat tct tta gaa gat ata gat aag ttt tta gaa gaa gca gat gat 3744
 Glu Asp Ser Leu Glu Asp Ile Asp Lys Phe Leu Glu Glu Ala Asp Asp
 1235 1240 1245

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<212> PRT

<213> Candida albicans

<400> 2

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 35 40 45

Val Phe Lys Lys Ala Ile Glu Leu Asn Gln Ile Asn Phe Phe Ala Met
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Cys Phe Thr Lys Leu Leu Ser Lys Val Leu Pro Leu Lys Arg Gly Val
 65 70 75 80

Leu Ala Gly Asp Arg Ile Val Lys Phe Cys Tyr Leu Phe Val Asn Gly
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Leu Val Lys Asp Ala Asn Glu Glu Lys Arg Ser Lys Glu Glu Glu Lys
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Glu Glu Lys Asp Lys Asp Glu Asp Lys Asp Thr Asn Glu Ser Asp Lys
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Asn Glu Glu Asp Gln Glu Asp Gln Glu Gly Glu Gly Asp Gln Glu Thr
 130 135 140

Pro Ile Ser Glu Phe Ile Ser Tyr Leu Ile Lys Tyr Leu Leu Ser Gly
 145 150 155 160

75183

Ile Glu Ala Lys Asp Lys Leu Val Arg Tyr Arg Val Val Gln Thr Leu
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Ala Tyr Leu Val Glu Phe Leu Thr Glu Ile His Glu Asn Asn Thr Leu
 180 185 190

Glu Ala Leu Tyr Thr Leu Leu Ser Asn Arg Leu Gln Asp Lys Glu Leu
 195 200 205

Ser Ile Arg Ile Gln Ala Val Val Ala Leu Ser His Phe Gln Leu Phe
 210 215 220

Glu Phe Ser Ile Glu Gly Asp Thr Gly Glu Phe Glu Asp Glu Leu Ile
 225 230 235 240

Ser Ser Asn Gln Ile Gln Asn Lys Leu Ile Asn Ser Ile Gln Asn Asp
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Asp Ser Pro Glu Val Arg Arg Ala Ala Leu Met Asn Leu Val Lys Thr
 260 265 270

Gln Asp Thr Ile Pro Ile Leu Leu Glu Arg Ala Arg Asp Ser Asn Ser
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Ile Asn Arg Arg Leu Val Tyr Ser Lys Ile Ala Arg Glu Leu Ile Thr
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Asp Leu Asp Asp Leu Glu Phe Glu Asp Arg Glu Phe Leu Leu Lys Trp
 305 310 315 320

Gly Leu Asn Asp Arg Asp Glu Thr Val Lys Ala Ala Ala Thr Lys Met
 325 330 335

Leu Thr Ile Tyr Trp Tyr Gln Ser Val Asn Glu Asp Leu Leu Glu Leu
 340 345 350

Ile Asp Gln Leu Asn Val Lys Ser Ala Ile Ala Glu Gln Ala Ile Leu
 355 360 365

Ala Phe Phe Lys Asn Lys Pro Glu Val Leu Glu Thr Ile Lys Ile Asp
 370 375 380

Glu Ser Tyr Trp Lys Asn Leu Thr Thr Glu Lys Ala Phe Leu Met Arg
 385 390 395 400

Thr Phe Tyr Gln Tyr Cys Asn Glu Asn Gln Leu His Ala Leu Met Asp
 405 410 415

76183

Ala Asn Phe Pro Glu Leu Leu Asp Leu Ser Ile Thr Leu Glu Lys Tyr
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Leu Ser Val Arg Leu Lys Thr Ile Asn Glu Asn Glu Asn Leu Val Lys
 435 440 445

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 450 455 460

Phe Ser Leu Glu Asn Gln Ile Ser Arg Ile Asn Thr Asp Ala Asp Asn
 465 470 475 480

Phe Arg Lys Ser Leu Ser Asn Ile Glu Glu Asp Ile Ile Glu Ile Asn
 485 490 495

Ile Ala Lys Asp Leu Phe Lys Lys Arg Ile Lys Gln Leu Lys Asn Asn
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Ser Gly Asn Leu Glu Asp Leu Ile Thr Glu Glu Asn Gln Glu Ile Ala
 515 520 525

Asp Gln Ile Lys Asp Phe Leu Met Glu Asp Leu Gln Gln Gln Leu Glu
 530 535 540

Asp Ile Asn Lys Asn Leu Asp Glu Ile Glu His His Pro Glu Asp Ile
 545 550 555 560

Thr Ala Lys Leu Glu Glu Leu Gln Thr Lys Tyr Asp Ser Cys Ile Arg
 565 570 575

Ala Leu Glu Thr Thr Ser Glu Leu Lys Ile Gln Thr Val Gln Ile Phe
 580 585 590

Glu Gln Glu His Glu Asn Asp Cys Ile Pro Phe Val Asp Ala Leu Lys
 595 600 605

Glu Leu Glu Phe Ile Ile Asn Gln Leu Leu Leu Ile Val Lys Asp Phe
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Asp Tyr Gly Asp Glu Met Ala Arg Arg Lys Leu Leu His Ile Ile Arg
 625 630 635 640

Met Thr Leu Thr Glu Asp Lys Leu Pro Asp Ala Leu Ile Ser Val Ala
 645 650 655

Leu Arg Val Leu Arg Ala Leu Ser Ile Asn Glu Lys Asp Phe Val Ser
 660 665 670

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Met Ala Val Glu Ile Ile Thr Asp Ile Arg Asp Ser Arg Asp Asp Glu
 675 680 685

Glu Phe His Ser Ala Ala Ala Thr Phe Asp Asp Asp Asp Asp Ile
 690 695 700

Leu Gly Asn Gly Asp Asp Glu Ser Gln Gln Ser Ser Ser Leu Ser Ala
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Val Thr Lys Lys Arg Arg Ile Glu Pro Asp Met Pro Pro Asp Asp Ile
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Val Leu Arg Cys Leu Thr Met Thr Gln Tyr Val Leu Glu Val Ile Thr
 740 745 750

His Ser Leu Asp Asp His Leu Ser Leu Ser Ser Ile Tyr Ser Gly Ile
 755 760 765

Val Asn Tyr Ala Ile Gln Asn Glu Ser Lys Lys Lys Leu Tyr Leu Ala
 770 775 780

Gly Leu Thr Cys Leu Gly Leu Tyr Ser Leu Ile Asp Ser Lys Ile Ala
 785 790 795 800

Arg Ile Ala Thr Thr Thr Leu Leu Leu Ala Met Arg Ser Asn Gly Glu
 805 810 815

Glu Val Lys Glu Ile Gly Met Lys Ala Ile Val Asp Ile Leu Ala Ile
 820 825 830

Tyr Gly Met Ser Ile Leu Asp Lys Ser Ser Lys Tyr Lys Tyr Ser Arg
 835 840 845

Met Phe Phe Lys Val Leu Asn Ser Phe Asp Ala Pro Lys Leu Gln Cys
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Ile Val Ala Glu Gly Leu Cys Lys Leu Phe Leu Ala Asp Ile Leu Tyr
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Lys Thr Asp Lys Arg Ser Leu Phe Gly Asn Ala Ile Gln Gly Gly Gly
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Gly Gly Gly Gly Gly Asn Asp Asp Pro Thr Thr Thr Asn Asp Asp Glu
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 915 920 925

78183

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 945 950 955 960

Asn His Gln Ile Asn Leu Ala Ala Val Ser Gly Asp Val Ile Tyr Arg
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 980 985 990

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 995 1000 1005

Glu Glu Ile Asn Gln Ala Thr Ser His Leu Trp Gln Cys Val Tyr Leu
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Ile Asn Asn Leu Asn Lys Phe His Ile Thr Glu Glu Leu Glu Ser Asn
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Gln Leu Gln Ala Leu Ile Lys Ala Leu Asp Ala Thr Val Glu Leu Phe
 1060 1065 1070

Thr Asn Asn Glu Asp Asn Pro Asn Phe Ile Leu Asp Lys Pro Thr Lys
 1075 1080 1085

Lys Asn Phe Asp Thr Phe Ile Glu Ser Ile Lys Asn Lys Leu Glu Ile
 1090 1095 1100

Ala Gln Lys Arg Glu Glu Asn Glu Leu Ile Lys Ser Gly Thr Asn Ser
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Ile Leu His Glu Leu Asp Asp Leu Asp Ile Gly Thr Gly Glu Ser Ser
 1125 1130 1135

Gln Ile Ser Ile Lys Ser Glu Thr Lys Arg Arg Asp Leu Asp Arg Ser
 1140 1145 1150

Leu Gln Val Ser Lys Thr Thr Ser Pro Glu Thr Ser Glu Asn Glu Asp
 1155 1160 1165

Glu Glu Asp Asp Asn Glu Glu Glu Glu Gln Glu Lys Lys Lys Ser Phe
 1170 1175 1180

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Thr Asp Gly Lys Asn Lys Leu Glu Leu Lys Ala Asp Lys Pro Ile Thr
185 1190 1195 1200

Phe Lys Ala Glu Asp Lys Arg Glu Gly Ser Val Glu Thr Asp His Gly
1205 1210 1215

Gln Glu Gln Val Leu Val Glu Ser Lys Lys Val Ile Asp Ser Asn Val
1220 1225 1230

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Val Asp Tyr Gly Asp Ile Ser Met Asp
1250 1255

80/83

SEQUENCE LISTING

<110> Hoechst Marion Roussel

<120> ESSENTIAL GENES FROM C. ALBICANS AND A METHOD FOR
SCREENING ANTIMYCOTIC SUBSTANCES USING SAID GENES

<130> SEQID14

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<141>

<160> 1

<170> PatentIn Ver. 2.1

<210> 1

<211> 603

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Homologous
fragment to Sc YDR325

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gatacaggaag atcaagaagg agaaggagat caagaaactc caatttcgga attcatatca 180
tatttgataa aatatttatt gagtgggata gaggctaaaag ataaactggg tcgttatcgt 240
gtgtacaaa cattagcata cttggttgaa ttcttgaccg agatacacga gaataatata 300
ttggaagcgt tatatacttt attaagtaat aggctacaag ataaagagct gtcgatacgt 360
attcaagctg ttgtggcatt atcacatttt caattatttg aatttagtat tgaaggatgat 420
actggagaat ttgaggatga attaatatca agtaacccaa ttcagaataa attgataaat 480
tccattcaaa atgatgatag tccagaagtc agacgtgcag cattaatgaa tttgggttaa 540
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aga 603
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81/83

SEQUENCE LISTING

<110> Hoechst Marion Roussel

<120> ESSENTIAL GENES FROM C. ALBICANS AND A METHOD FOR
SCREENING ANTIMYCOTIC SUBSTANCES USING SAID GENES.

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<211> 581

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Homologous
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tgctatagct gaacaggcca tattagcatt ttttaaaaat aaaccagaag ttcttgcaac 180
tattaaaatt gatgaatcat attggaaaaa tctaactaca gaaaaggcat tcttgatgag 240
gacgttttat caatattgta atgagaatca attacatgct ttaatggatg ccaatttccc 300
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aaatgaaaat gaaaatttaa ttaagacatg ggaaacttat aatgccaaga ttgacgaatt 420
agatgatcaa atatttagtc ttgaaaacca gatttccaga ataaatactg atgccgataa 480
tttccgtaaa agtttatcta acattgaaga agatattatt gaaatcaata ttgctaagga 540
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82/83

SEQUENCE LISTING

<110> Hoechst Marion Roussel

<120> ESSENTIAL GENES FROM C. ALBICANS AND A METHOD FOR
SCREENING ANTIMYCOTIC SUBSTANCES USING SAID GENES

<130> SEQID16

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<160> 1

<170> PatentIn Ver. 2.1

<210> 1

<211> 662

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Homologous
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attcaagggtg gtggtggtgg tgatgatcca actaccacca atgacgatga aactgaagaa 180
gaaacagatc gagagcatga aaagcattta tttgaagcga ttgtacttat ttatttcaac 240
cccaacacca aatcaaatca agaattacaa caaattttgt cattttgtat tccagtttat 300
gcctttttctc atataaatca tcaaatcaat ttagctgcag ttagtggtga tgttatttat 360
cgacttttca ctgaaacaga aacagaatta tcaccaagtg ttataatccc tcaattaata 420
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tcacatttat ggcaatgtgt ttatttatta caagtgggtg aacaagtaga tgctcgtaat 540
gttaaaagat gcatcattaa caatttgaat aaatttcata taacggaaga attagaatca 600
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83/83

SEQUENCE LISTING

<110> Hoechst Marion Roussel

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ttcattatcc aaatttggtta gagatggcga agataaaacc aatcatacta ttcaatggaa 180
aattgtcatg aatggtaatt gtgaattctt gacacagggt gaagaaatga a          231
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